

NUKLEINSÄUREARRAY BESTEHEND AUS SELEKTIVEN MONOZYTEN-MAKROPHAGEN-GENE

Beschreibung

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Die Erfindung betrifft einen Array bestehend aus Oligo- oder Polynukleotidsonden, die immobilisiert auf einen festen Träger aufgebracht sind. Das Array ist dadurch charakterisiert, dass auf der Oberfläche Sequenzen einer Auswahl oder aller der in den Tabellen 1-6 genannten selektiven Monozyten-Makrophagen-Gene gebunden sind. Dieser Nukleinsäure-Array ermöglicht die Diagnose der rheumatoiden Arthritis, eine begleitende Analyse der Behandlungseffektivität und die Überwachung von Nebenwirkungen bei der anti-Tumornekrosefaktor-(TNF)-Therapie und somit die Auswahl der für den jeweiligen Patienten mit rheumatoider Arthritis am wirkungsvollsten Therapie. Die vorliegende Erfindung betrifft ferner einen Nukleinsäure-Array zur Prognose und zur Entwicklung neuer anti-TNF gerichteter Pharmaka oder solcher Pharmaka, die in dessen Regelkreis eingreifen.

Die Zellen des Monozyten / Makrophagen-Systems sind an der Aktivierung und Aufrechterhaltung von Entzündungskaskaden im Blut und im Gewebe z. B. im Rahmen der rheumatoiden Arthritis und bei anderen chronisch entzündlichen Erkrankungen, aber auch bei autoaggressiven Erkrankungen wesentlich beteiligt. Bei diesen Erkrankungen sind Monozyten und Makrophagen hoch aktiviert, zeigen Veränderungen im Besatz ihrer Oberflächen-Moleküle, treten mit anderen Zellen in Kontakt und sezernieren bestimmte Botenstoffe wie u. a. TNF-alpha, die dafür sorgen, den Entzündungsvorgang zu unterhalten. TNF-alpha ist ein von Monozyten / Makrophagen, Lymphozyten und Mastzellen gebildetes Zytokin mit Einfluss auf Entzündung, Sepsis, Lipid- und Proteinstoffwechsel, Blutbildung, Angiogenese, Wund-

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heilung und Immunabwehr, das aber auch zytolytische bzw. zytostatische Wirkung auf Tumorzellen hat.

Bei entzündlichen Erkrankungen zeigen Monozyten
5 Makrophagen ein charakteristisches, pathologisch verändertes Genexpressionsmuster mit deutlichen Abweichungen im Vergleich zu gesunden Probanden. Mit dem Fachmann bekannten bioinformatischen Methoden wie z. B. der Signifikanz- und Clusteranalyse lassen sich u. a. Gene mit ähnlichem Verhalten und hoch- oder niederregulierte Gene aus
10 den Hybridisierungsmustern eines Nukleinsäurearrays bestimmen.

Die zunehmende Verfügbarkeit der Hochdurchsatz-Verfahren
15 in Form von Nukleinsäurearrays, die exponentiell anwachsenden Informationen zum humanen Genom und der Genexpression, sowie die globale Vernetzung von Datenbanken mit strukturierten biomedizinischen Informationen wird die Betrachtungsweise chronisch entzündlicher und entzündlich-rheumatischer Krankheitsbilder grundlegend verändern. Aus dem verbesserten Verständnis der molekularen Grundlagen der zell-, gewebs- und krankheitsspezifischen Genexpression lassen sich die molekularen Abläufe definieren und tragen dazu bei, eine frühere Diagnose und
20 verbesserte Prognose zu erlauben. Zum anderen gewährleisten Mikroarray-Technologien effektivere Therapieformen für die rheumatoide Arthritis und für andere chronisch entzündliche Erkrankungen zu entwickeln und ermöglichen ein schnelles Screeningsystem. Ferner erlauben diese multiplen Verfahren die Entwicklung von pharmazeutischen und biologisch wirksamen Medikamenten (Biologicals) zu beschleunigen und die Testphasen der Medikamentenwirkung, wie auch die Beurteilung der Medikamenten Nebenwirkungen schneller beurteilen zu können. Aus diesem Grund stellt
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dieses Verfahren einen volkswirtschaftlichen und wirtschaftlichen Gewinn dar.

Die Mikroarray Technologie stellt eine Miniaturisierung
5 analytischer Verfahren auf der Basis der DNA- bzw. RNA-
Hybridisierung im Hochdurchsatz-Verfahren dar. Gleichzeitig
können dadurch viele tausend verschiedene DNA/DNA-
(DNA/RNA-) Wechselwirkungen innerhalb eines Testansatzes
analysiert werden. mRNA-Expressionsprofile werden mittels
10 DNA-Arrays durch die Hybridisierung von markierten cRNA
oder cDNA-Proben bestimmt. Diese Technologien erfordern
ein hohes Maß an Automatisierung und Standardisierung mit
Aufbau und Nutzung entsprechender Proben- und Datenbanken
(Sequenzinformationen, Oligonukleotide). Die derzeit ver-
15 wendeten DNA-Arrays unterscheiden sich im Trägermaterial
(Nylonmembranen, Glasoberflächen, Edelmetall bedampfte
Glasoberflächen, Kunststoffe), der Länge bzw. der Her-
stellung der an den Träger immobilisierten DNA-Sequenzen
und der Markierungstechnik für eine zu bindende Probe. In
20 Analogie zu den Methoden der DNA-Hybridisierung beim Sou-
thern-/Dot-Blot können DNA-Sequenzen auf einem Filter
punktförmig und in systematischer Reihenfolge mit einem
Druckkopf durch Spotting, durch Piezo-Druckverfahren
(Tintenstrahltechnologie) oder durch Photolithographie
25 (chemische Direktsynthese auf dem Trägermaterial) fixiert
werden. Die DNA kann dabei eine cDNA, ein PCR-Produkt o-
der ein synthetisch hergestelltes Oligonukleotid sein.
Jede dieser aufgetragenen Sequenzen ist damit einem spe-
zifischen Ort in einer bekannten Anordnung zugeteilt. Aus
30 einer klinischen oder aber pharmazeutisch zu untersuchen-
den Probe kann RNA aufgereinigt werden und nach Umschrei-
bung durch reverse Transkription mit den auf dem Array
befindlichen komplementären Nukleinsäurensträngen die in
einer hohen genomweiten Anzahl oder aber einer bereits

vorselektionierten Anzahl aufgebracht sind hybridisiert werden. Die Markierung der Probe erfolgt dabei mittels eingebauter radioaktiver Nukleotide, über Biotin-Streptavidin Wechselwirkungen, Digoxigenin-Enzym Verstärkungen oder aber über direkte oder indirekte eingebaute Fluoreszenzfarbstoffe. Das Auslesen der Information erfolgt über die Intensität der Radioaktivität oder der Fluoreszenz an einem spezifischen Ort des Trägermaterials und lässt somit Rückschlüsse zu, welche relative Menge an spezifisch gebundener DNA- bzw. RNA-Sequenz in der markierten Probe vorhanden war.

Das An- und Abschalten von Genen ist Grundlage aller biologischen Prozesse und außerdem eine extrem sensitive Antwort auf veränderte äußere Bedingungen. Mit der Extraktion von RNA aus einer biologischen Probe, dem Einwirken von markierter cDNA oder RNA auf einen Nukleinsäure-Array (Hybridisierung) und dessen Analyse ist innerhalb kürzester Zeit eine große Fülle von Informationen über den Zustand der Zellen in der biologischen Probe unter veränderten Bedingungen möglich. Die auf der Hybridisierung von Nukleinsäuren beruhende Technologie hat den Vorteil einer extrem hohen Spezifität, Sensitivität und relativ leichten, schnellen Durchführbarkeit.

Geschieht das An- oder Abschalten von Genen in Monozyten/Makrophagen in nicht physiologischer Weise, so kann es die Ursache von entzündlichen Erkrankungen oder ein messbares Zeichen für diese sein. Die Therapie mit anti-TNF wirksamen Medikamenten sollte im Idealfall die pathologisch veränderte Genexpression in den betroffenen Zellen auf das Niveau von gesunden Patienten normalisieren.

Durch Untersuchung der Genexpressionsprofile ist zu erwarten, dass eine neue molekulare Charakterisierung der rheumatoiden Arthritis und anderer chronisch entzündlicher Erkrankungen möglich wird und damit eine Einteilung in Subgruppen nach pathophysiologischen Besonderheiten erfolgt. Bei den entzündungshemmenden anti-TNF Therapien stehen somit prognostische Vorhersagen in Aussicht über die Aggressivität im weiteren Verlauf. Dies würde bereits frühzeitig Einfluß auf die Wahl und Intensität der medikamentösen Therapie mit den bisher bekannten bei chronischen Entzündungen verwendeten Medikamenten, aber auch mit biologisch wirksamen TNF-Blockern ausüben. Zum anderen ergeben sich hieraus weitere Ansatzpunkte, um die Therapieform im Hinblick auf die potentiellen Nebenwirkungen durch Einflussnahme dieser Medikamente zu gestalten und die Auswirkung der Nebenwirkungen rechtzeitig abzuschätzen.

Durch anti-TNF gerichtete Therapien bei der rheumatoiden Arthritis und anderen chronisch entzündlichen oder autoaggressiven Erkrankungen wird zum einen eine potentielle Entstehung neoplastischer Veränderungen bis hin zur Tumorbildung diskutiert, zum anderen vermindert die anti-TNF Therapie die Immunabwehr, sodass bei den behandelten Patienten vermehrt Infektionen auftreten, u. a. Tuberkulose.

Mit Hilfe von Nukleinsäure-Array-Systemen kann die Expression tumorrelevanter Gene im Verlauf der anti-TNF Behandlung überprüft und somit frühzeitig Hinweise auf mögliche neoplastische Veränderungen geben, so dass einer beginnenden Tumorentwicklung rechtzeitig entgegengesteuert und die anti-TNF Therapie entsprechend angepasst oder falls nötig abgebrochen werden kann.

Der Erfindung liegt die Aufgabe zugrunde, Mittel zur Überwachung der Wirksamkeit sowie von Nebenwirkungen der anti-TNF Therapie zu schaffen, aber auch die Feindiagnostik einer entzündlichen Erkrankung und damit die Auswahl der für den jeweiligen Patienten effektivsten Therapieform zu ermöglichen. Eine weitere Aufgabe der vorliegenden Erfindung besteht darin, die Wirksamkeit und Nebenwirkungen neuer anti-TNF gerichteter Pharmaka im Rahmen von klinischen Studien zu verfolgen. Erfindungsgemäß wird ein neuer Array geschaffen bestehend aus Oligo- oder Polynukleotidsonden, die immobilisiert auf einem festen Träger aufgebracht sind. Verglichen mit bisher bekannten genomweiten DNA-Chips ist der Vorteil der Erfindung eine Kostenersparnis bei der Herstellung des Nukleinsäurearrays, weil es überwiegend nur Gene enthält, die zur Lösung der Aufgabe der Erfindung interessant sind, was den Aufwand der Datenauswertung minimiert und damit verbillicht.

Erfindungsgemäß wird die Aufgabe durch einen Nukleinsäure-Array gelöst, auf dessen Oberfläche Sequenzen einer Auswahl oder aller der in den Tabellen 1 bis 6 genannten selektiven Monozyten-Makrophagen-Gene aufgebracht sind. Anhand des Gen- oder Sequenznamens oder der Accession-Nummer kann die Sequenz aus öffentlich zugänglichen Datenbanken, vorzugsweise GeneBank oder EMBL, ermittelt werden. Die Sequenzen der aus dem Array befindlichen Nukleinsäuren können aus Genen bestehen, deren Expressionsniveau durch eine anti-TNF wirksame Therapie verändert wird.

Gegebenenfalls können auf dem erfindungsgemäßen Nukleinsäure-Array weitere Gene vorhanden sein, vorteilhaft sol-

che, von denen bekannt ist, dass sie in jeder Zelle
exprimiert werden und zur Grundausstattung der Zelle ge-
hören. Die Gene, die für diese Nukleinsäuren codieren,
werden üblicherweise als Haushalts- oder Housekeeping-
5 Gene bezeichnet und werden zur Normierung der erhaltenen
Signale verwendet. Das Array kann die genannten Sequen-
zen in Form von DNA, komplementärer RNA oder chemisch
modifizierten Nukleinsäuren, vorzugsweise PNA (protein
nucleic acid) enthalten.

10 Bei den Genen oder Gensequenzen kann es sich um krank-
heits- und nebenwirkungsrelevante selektionierte Gene der
rheumatoiden Arthritis oder anderer chronisch entzündli-
cher Erkrankungen handeln, vorzugsweise aus dem Monozy-
15 ten/Makrophagen-Zellsystem. Gegebenenfalls können auf
den Oberfläche des Arrays auch Allele, Derivate und/oder
Splicingvarianten der Gen- oder Genteilsequenzen oder O-
ligomersequenzen vorliegen. Die Übereinstimmung der Se-
quenzen auf dem Array mit den entsprechenden Sequenzen in
20 Tabelle 1-6 soll dabei mindestens 80 % in den Protein-
kodierenden Abschnitten der mRNA betragen.

Der Träger, auf den die Nukleinsäuren aufgetragen werden,
kann jeder Träger sein, der normalerweise für RNA- oder
25 DNA Arrays verwendet wird. Die Verfahren zum Auftragen
und Immobilisieren der Nukleinsäuren sind Stand der Tech-
nik und dem Fachmann bekannt. Zur Kopplung der genannten
Sequenzen kann der Träger mit reaktiven Gruppen, Metall-
verbindungen oder Legierungen beschichtet sein. Die Gene
30 oder Gensequenzen können beispielsweise durch Spottingver-
fahren, Immobilisierungsverfahren oder durch in-sito Syn-
theseverfahren von Oligomeren oder spiegelbildlich in
Form von RNA aufgebracht werden.

Das erfindungsgemäße Array kann beispielsweise zur Messung der Monozyten/Makrophagen Aktivierung oder der Entzündungsaktivität im Blut oder Zellgewebe bei entzündlichen Erkrankungen, vorzugsweise der rheumatoiden Arthritis verwendet werden. Das Array kann z. B. zur Früherkennung der genannten Erkrankungen bei genetisch vorbelasteten Patienten verwendet werden, noch bevor sich klinische Symptome manifestieren. Ein weiterer Einsatzbereich ist die Feindiagnostik, vorzugsweise die Einteilung von Patienten in Subgruppen, die jeweils eine unterschiedliche Therapie und unterschiedliche Medikamente benötigen. Das Array kann ferner zur Therapieüberwachung, zur Verfolgung von Nebenwirkungen, zur Erstellung einer Prognose und zur Identifizierung neuer pharmazeutischer Targets bei den genannten Erkrankungen verwendet werden.

Dazu werden den zu untersuchenden Patienten Blut oder Gewebeproben entnommen, aus denen RNA mit bekannten Standardtechniken isoliert und gegebenenfalls als Gesamt-RNA oder Poly A+-RNA weiterverwendet wird. Mit reverser Transkriptase kann die RNA in cDNA umgeschrieben und dabei mit einer Markierung versehen werden, z. b. einem Fluoreszenzfarbstoff, einem radioaktiven Nuklid oder einem Enzym wie alkalische Phosphatase. Daneben kann die RNA direkt markiert oder unmarkiert zur Hybridisierung des Nukleinsäure-Arrays eingesetzt werden. Nach Hybridisierung des Arrays mit den Nukleinsäureproben und nachfolgenden Waschschritten kann die Bindung der Probe an die auf dem Array befindlichen Sequenzen mit jedem geeigneten Verfahren analysiert werden. Im Falle einer Fluoreszenzmarkierung sind dies optische Verfahren, bei radioaktiv markieren Proben käme eine Autoradiographie zur Anwendung und bei einer Enzymmarkierung entzymatische

Nachweisverfahren, z. B. die Umsetzung eines farblosen Substrates zu einem farbigen Produkt.

Ein inverser Nachweis von festphasengebundener Total- oder mRNA mit den Sequenzen aus Tabelle 1-6 ist ebenfalls möglich. Dazu werden auf den RNA-Mikroarrays Blut- oder gewebsspezifische RNA-Moleküle von bis zu 500 Patienten gebunden. Der qualitative / quantitative Nachweis der Transkriptmenge relevanter Gene erfolgt dann mit den in Tabelle 1-6 beschriebenen selektionierten Genen, Genabschnitten oder Oligomeren. Die RNA-Proben werden auf Kopplungsträger gespottet und setzen sich aus Total-RNA oder messenger-RNA zusammen. Die RNA dient dabei als Target für die aus DNA-Mikroarrays abgeleiteten hoch signifikant exprimierten Gene nach Tabelle 1-6, die als markierte Sonden zur Hybridisierung eingesetzt werden. Vorgeschlagen wird das Koppeln biotinylierter RNA oder messenger-RNA auf Streptavidin beschichteten Glasträgern (Slides). Nach Markierung der RNA mit Biotinderivaten, wird die RNA auf Poly-L-Lysin behandelten vorzugsweise aber auf mit Streptavidin beschichteten Glas- oder Plastikslides durch Spotting aufgebracht und getrocknet. Eine Degradation der RNA wird so verhindert. Alternativ bietet sich eine kovalente Kopplung der RNA durch Bindung an reaktive Trägermaterialien an, die vorzugsweise durch UV-Bestrahlung katalysiert wird. Zusätzlich ist eine multiple, gleichzeitige Markierung verschiedener Gene, Geneinheiten oder Oligomere mit verschiedenen Markierungsspezies, z.B. Radioaktivität, Fluoreszein, Digoxigenin und enzymatischen Markierungen vorteilhaft.

Parallel unterschiedliche Markierungen der Sonden mit unterschiedlichen Fluoreszenzfarbstoffen sind möglich. Alternativ sind enzymatische oder aber radioaktive Sonden-

markierungen zu nennen. Zur Quantifizierung und Qualitätskontrolle werden markierte Haushaltsgene (alpha-, beta, gamma-Aktin, GAPDH usw.) eingesetzt. Bevorzugt wird der Nachweis hier parallel und gleichzeitig mit maximal 50 Gensonden pro Ansatz gleichzeitig durchgeführt.

Neben der Vereinfachung der biometrischen Analyse durch Kopplung von RNA Spezies an Trägermaterialien erlaubt dieses System eine schnelle Diagnostik und bietet eine komplexe für den Patienten individuell schnelle Diagnostik, Prognostik und Therapiesteuerung. Insbesondere bei pharmakologischen Entwicklungsstrategien erlaubt das System eine schnelle Durchführung mit hohem Durchsatz.

Die folgenden Beispiele und Abbildungen dienen nur zur Erläuterung und beschränken in keiner Weise den Umfang der Erfindung.

1. Isolierung von Monozyten

Im hier angewandten Verfahren wurde die Auswahl selektiver hochreiner Monozyten des peripheren Blutes benutzt, um eine Aussage 1.) zur Krankheitsspezifität, 2.) der Anwendung des Therapeutikums anti-TNF-alpha, als "Biological", 3.) im Vergleich zum Gesunden Probanden, als auch 4.) zur Bewertung von anti-TNF-alpha relevanten gendiagnostischen Möglichkeiten, zu ermöglichen. Dabei wurden die peripheren Blut-Leukozyten aus peripherem Blut durch eine Fikollgradienten-Dichtezentrifugation angereichert. Diese Fraktion, die individuell unterschiedliche Zusammensetzung aus Monozyten (5-12%), CD4+ T-Zellen (85-92 %), CD8+ T-Zellen (5-10%), NK-Zellen (2-5%), basophilen und neutrophilen Granulozyten aufweist, wurde zur Gewinnung spezifischer Monozytenfraktionen weiteren Reinigungsschritten unterzogen. Hierbei kamen sowohl Negativ-

selektionen, bei denen sämtliche andere Zellfraktionen über magnetische Beads-Antikörper Wechselwirkungen entfernt werden, als auch Positivselektionen durch CD14+ Markierung über magnetische Beads oder aber FACS Zellsortierungsverfahren zum Einsatz. Bei beiden Verfahren ergaben sich Monozyten-Zellreinheiten von ca. 96 %.

2. RNA-Gewinnung

Die reinen Monozytenfraktionen wurden in RNA-Lysepuffer aufgenommen und die RNA dann über einen kommerziell erhältlichen RNA Reinigungskit (Qiagen) gereinigt. Die RNA wurde über etablierte cDNA Umschreibemethoden durch reverse Transkription in cDNA umgeschrieben und dann einem weiteren linearen Amplifikationsschritt durch das angewandte "Eberwine Protokoll" zur Herstellung von aRNA (amplifizierte RNA) unterzogen. Die Quantität und Qualität der RNA, cDNA, und aRNA wurde jeweils durch Gelelektrophorese, photometrische Bestimmung und über Messungen mit dem Bioanalyzer 2100 (Fa. Agilent) verifiziert.

3. Affymetrix Chip Hybridisierung

Für Expressionsanalysen werden im System der Firma Affymetrix spezifische direkt aus Datenbanksequenzen abgeleitete Oligonukleotide als DNA-Proben verwendet. Diese werden auf dem Array mit Targets aus fluoreszenz-markierten revers transkribierten Proben in Form von cDNA oder mit linear amplifizierten Proben in Form von aRNA hybridisiert.

Die Hybridisierung des genomweiten Affymetrix-Arrays (U-133A) und weitere Bearbeitung erfolgt maschinell unter Standardbedingungen nach Angaben des Herstellers Affymetrix in einem speziellen Hybridisierungs- und Waschgerät mit den speziellen Puffern. Genexpressionsmuster

werden nach Hybridisierung über das Verhältnis der Fluoreszenzintensitäten bei einer bestimmten Wellenlänge erstellt. Solche Hochdurchsatz-Expressionsanalysen erlauben Vergleiche der Expressionsmengen von Genen gleichzeitig in gesundem und krankem Personen oder Vergleiche der Genexpression vor und nach Arzneimittelzugabe zur Risikoabschätzung (Pharma-/Toxikogenomik), zur Feindiagnostik und Abschätzung der Komplexität von Erkrankungen.

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4. Datenauswertung

Zum Einsatz kamen dabei aRNA Proben aus peripheren Blut-Monozyten 1.) gesunder Blutspender, 2.) chronisch aktiver Patienten mit rheumatoider Arthritis vor Behandlung und 3.) nach Behandlung mit TNF-alpha Antikörpern. Der Behandlungserfolg wurde über laborklinisch eindeutige Parameter und nach den klinisch anzuwendenden Kriterien der internationalen gültigen Parameteruntersuchungen (ACR-Kriterien) abgeschätzt. Ziel und Zweck dieser Dreigruppenuntersuchung war es, charakteristische Genexpressionen in folgenden Gruppensdefinitionen festzustellen:

1. Eine genregulatorische Krankheitsspezifität bei der aktiven unbehandelten rheumatoiden Arthritis, im Vergleich zur Genexpression gesunder Probanden.

2. Eine genregulatorisch spezifische Interpretation der anti-TNF-alpha-Behandlung zu charakterisieren und eine Bewertung der Behandlung im Vergleich zur Genexpression der aktiven unbehandelten Krankheit und im Vergleich zur Genexpression der gesunden Probanden durchzuführen.

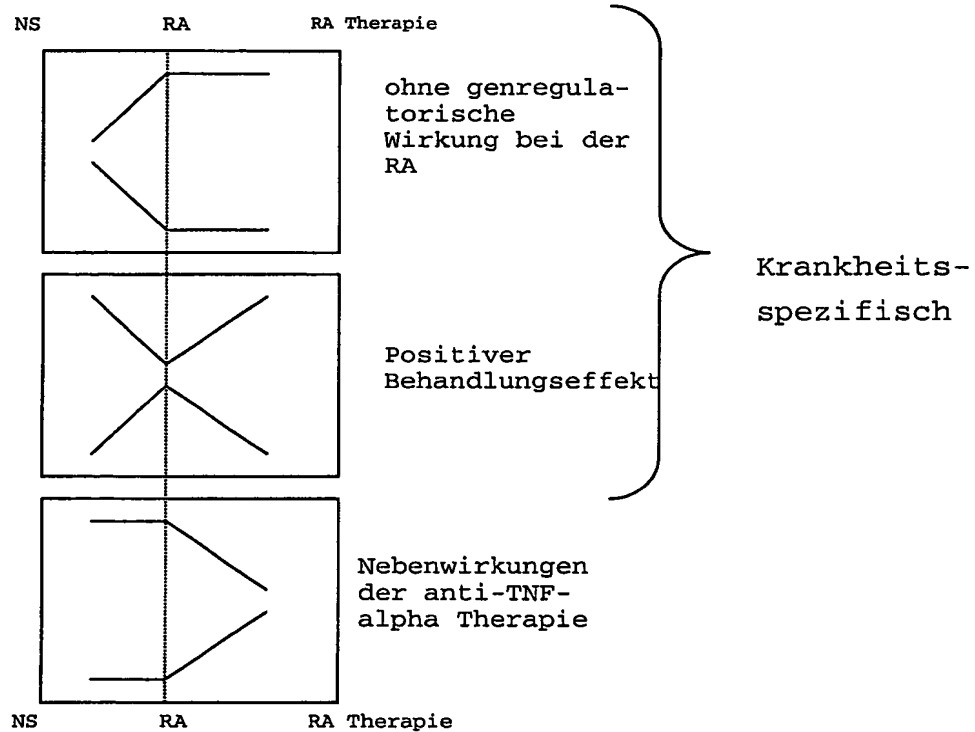
3. Die Bewertung von Nebenwirkungen durch das Medikament="Biological" anti-TNF zu gewährleisten. Hierbei wurde die spezifische Genexpression der anti-TNF-alpha behandelten Patienten mit rheumatoider Arthritis mit der Genexpression der unbehandelten selben Patienten, und der von gesunden Blutspender verglichen.

Die Bearbeitung und Messung der einzelnen Genexpressionen innerhalb des genomweiten humanen Affymetrix-Arrays (U-133A) erfolgte innerhalb des zugehörigen Affymetrix Hybridisierungs-/ Wasch- und Auslesegerät - System. Die Auswertung vollzieht sich in 4 Schritten:

1. Bestimmung der bei der Expressionsanalyse detektierten signifikanten Gene, z. B. durch die „Fold-Change Method“ oder SAM („Significance Analysis of Microarrays“).
2. Separation der signifikanten Gene in verschiedene Sub-Populationen auf der Grundlage der Untersuchung der Expressionseigenschaften dieser Gene mittels Cluster-Analyse mit Verfahren wie „Hierarchical Clustering“, „Self-Organizing Maps“ oder „k-Means-Clustering“.
3. Auswertung des Verhaltens der signifikanten Gene innerhalb der Cluster unter Einbeziehung der klinischen Informationen (rheumatoide Arthritis (RA), anti-TNF-Therapie) und nach den Erfahrungswerten von Spezialisten.

4. Zuordnung der beteiligten Gene nach biologischen Pathways.

Allgemeines Verhalten der signifikanten Gene innerhalb der Cluster:



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Abb. 1: schematische Darstellung der Clusteranalyse

- 10 Das Genexpressionsverhalten eines gesunden Normalspenders (NS) sowie und eines aktiven Patienten mit rheumatoider Arthritis (RA) vor und nach einer anti-TNF-alpha Therapie wurden mittels Clusteranalyse verglichen. Die Ergebnisse sind in den Abbildungen 1 und 2 dargestellt.

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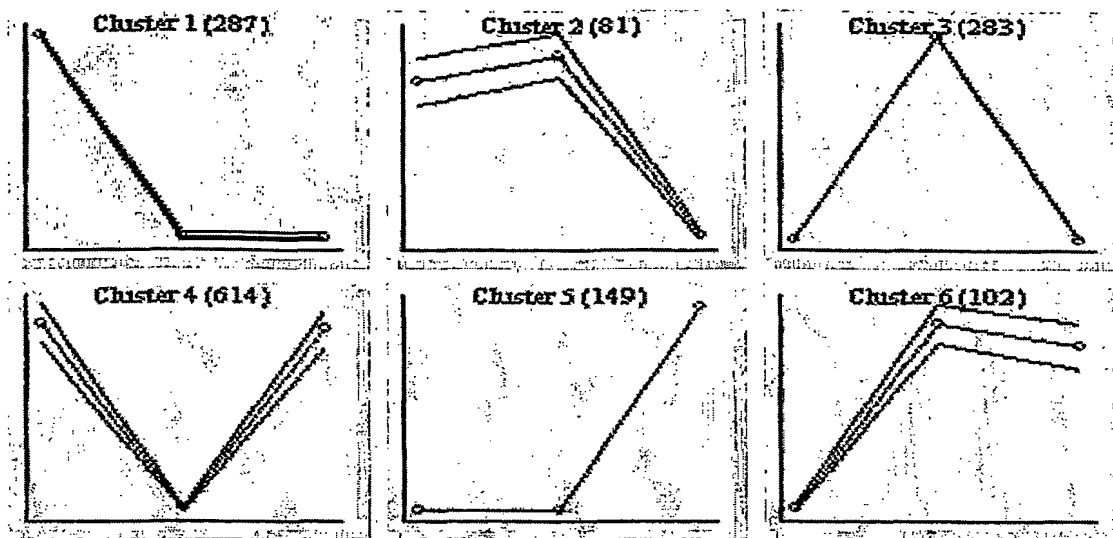


Abb. 2: Clusteranalyse anhand realer Daten.

Dargestellt sind die Genexpressionen der Clusteranalyse (n=6 Cluster). Die Anzahl der beteiligten Gene ist in Klammern wiedergegeben. Als Ergebnis der Clusteranalyse erhält man zusätzlich zum durchschnittlichen Genexpressions-Verhalten aller in einem Cluster befindlichen Gene ein Vertrauensintervall.

Die Cluster weisen dabei folgende Charakteristiken auf:

CLUSTER-1: Die krankheitsspezifische Genexpression ist kleiner im Vergleich zum Gesunden, die anti-TNF-Behandlung ist hier ohne genregulatorische Wirkung.

CLUSTER-2: Nebenwirkungen: Dargestellt durch die Medikamentenwirkung der Anti-TNF-alpha Behandlung besteht eine verminderte Expression der zugehörigen Gene beim behandelten Patienten.

CLUSTER-3: Die krankheitsspezifische Genexpression größer im Vergleich zum Gesunden. Die anti-TNF-alpha Behandlung zeigt einen positiven Effekt.

CLUSTER-4: Die krankheitsspezifische Genexpression ist kleiner im Vergleich zum Gesunden. Die anti-TNF-Behandlung zeigt einen positiven Effekt.

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CLUSTER-5: Nebenwirkungen: Dargestellt durch die Medikamentenwirkung der anti-TNF-alpha Behandlung besteht eine erhöhte Expression der zugehörigen Gene beim behandelten Patienten.

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CLUSTER-6: Die krankheitsspezifische Genexpression ist größer im Vergleich zum Gesunden. Die anti-TNF-alpha Behandlung ist hier ohne genregulatorische Wirkung.

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In den Tabellen 1-6 sind die in den oben beschriebenen Clustern enthaltenen Gene zusammen mit der Affymetrix Bezeichnung (links) und ihrer definierten GeneBank-Accession Nummer inkl. einer Beschreibung aufgeführt.

Tabelle 1: Gene aus Clusteranalyse 1

Affymetrix-interne Bezeichnung	Beschreibung der Sequenz in der GeneBank Datenbank
211554_x_at	gb:M17565.1 /DEF=Human MHC class II DQ-beta associated with DRw6, DQw1 protein, complete cds. /FEA=mrna /GEN=HLA-DQB1 /DB_XREF=gi:188188 /FL=gb:M17565.1
213831_at	Consensus includes gb:X00452.1 /DEF=Human mRNA for DC classII histocompatibility antigen alpha-chain. /FEA=mrna /PROD=DC classII histocompatibility antigenalpha-chain /DB_XREF=gi:32265 /UG=Hs.198253 major histocompatibility complex, class II, DQ alpha 1
212203_x_at	Consensus includes gb:BF338947 /FEA=EST /DB_XREF=gi:11285367 /DB_XREF=est:602036012F1 /CLONE=IMAGE:4184090 /UG=Hs.182241 interferon induced transmembrane protein 3 (1-8U)
209480_at	gb:M16276.1 /DEF=Human MHC class II HLA-DR2-Dw12 mRNA DQw1-beta, complete cds. /FEA=mrna /GEN=HLA-DRB2 /DB_XREF=gi:188397 /UG=Hs.73931 major histocompatibility complex, class II, DQ beta 1 /FL=gb:M60028.1 gb:M17564.1 gb:M81140.1 gb:M81141.1 gb:M16276.1 gb:NM 002123.1
218345_at	gb:NM_018487.1 /DEF=Homo sapiens hepatocellular carcinoma-associated antigen 112 (HCA112), mRNA. /FEA=mrna /GEN=HCA112 /PROD=hepatocellular carcinoma-associated antigen 112 /DB_XREF=gi:8923717 /UG=Hs.12126 hepatocellular carcinoma-associated antigen 112 /FL=gb:AF259340.1 gb:NM 018487.1
221491_x_at	Consensus includes gb:AA807056 /FEA=EST /DB_XREF=gi:2876632 /DB_XREF=est:oc35c12.sl /CLONE=IMAGE:1351702 /UG=Hs.279930 major histocompatibility complex, class II, DR beta 3 /FL=gb:M27635.1 gb:NM_022555.1 gb:M26038.1 gb:U95989.1 gb:U95819.1 gb:U66825.1
211734_s_at	gb:BC005912.1 /DEF=Homo sapiens, Fc fragment of IgE, high affinity I, receptor for; alpha polypeptide, clone MGC:14507, mRNA, complete cds. /FEA=mrna /PROD=Fc fragment of IgE, high affinity I, receptor for; alpha polypeptide /DB_XREF=gi:13543505 /FL=gb:BC005912.1
201330_at	gb:NM_002887.1 /DEF=Homo sapiens arginyl-tRNA synthetase (RARS), mRNA. /FEA=mrna /GEN=RARS /PROD=arginyl-tRNA synthetase /DB_XREF=gi:4506428 /UG=Hs.180832 arginyl-tRNA synthetase /FL=gb:BC000528.1 gb:NM 002887.1
201114_x_at	gb:NM_002792.1 /DEF=Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 7 (PSMA7), mRNA. /FEA=mrna /GEN=PSMA7 /PROD=proteasome (prosome, macropain) subunit, alpha type, 7 /DB_XREF=gi:4506188 /UG=Hs.233952 proteasome (prosome, macropain) subunit, alpha type, 7 /FL=gb:BC004427.1 gb:AF022815.1 gb:AF054185.1 gb:NM 002792.1
213418_at	Consensus includes gb:NM_002155.1 /DEF=Homo sapiens heat shock 70kD protein 6 (HSP70B), mRNA. /FEA=CDS /GEN=HSPA6 /PROD=heat shock 70kD protein 6 (HSP70B) /DB_XREF=gi:4504514 /UG=Hs.3268 heat shock 70kD protein 6 (HSP70B) /FL=gb:NM 002155.1
208961_s_at	gb:AB017493.1 /DEF=Homo sapiens mRNA for DNA-binding zinc finger (GBF), complete cds. /FEA=mrna /PROD=DNA-binding zinc finger (GBF) /DB_XREF=gi:3582142 /UG=Hs.285313 core promoter element binding protein /FL=gb:BC000311.1 gb:BC004301.1 gb:AF001461.1 gb:AB017493.1 gb:NM 001300.2
217753_s_at	gb:NM_001029.1 /DEF=Homo sapiens ribosomal protein S26 (RPS26), mRNA. /FEA=mrna /GEN=RPS26 /PROD=ribosomal protein S26 /DB_XREF=gi:4506708 /UG=Hs.299465 ribosomal protein S26 /FL=gb:BC002604.1 gb:NM 001029.1
201403_s_at	gb:NM_004528.1 /DEF=Homo sapiens microsomal glutathione S-transferase 3 (MGST3), mRNA. /FEA=mrna /GEN=MGST3 /PROD=microsomal glutathione S-transferase 3 /DB_XREF=gi:4758713 /UG=Hs.111811 microsomal glutathione S-transferase 3 /FL=gb:BC000505.1 gb:BC003034.1 gb:AF026977.1 gb:NM 004528.1
203103_s_at	gb:NM_014502.1 /DEF=Homo sapiens nuclear matrix protein NMP200 related to splicing factor PRP19 (NMP200), mRNA. /FEA=mrna /GEN=NMP200 /PROD=nuclear matrix protein NMP200 related to splicing factor PRP19 /DB_XREF=gi:7657380 /UG=Hs.173980 nuclear matrix protein NMP200 related to splicing factor PRP19 /FL=gb:NM 014502.1
221903_s_at	Consensus includes gb:BE046443 /FEA=EST /DB_XREF=gi:8363496 /DB_XREF=est:hn47d10.x2 /CLONE=IMAGE:3026803 /UG=Hs.18827 KIP40849 protein

217379_at	Consensus includes gb:AL121934 /DEF=Human DNA sequence from clone RP11-209A2 on chromosome 6. Contains an RPL10 (60S ribosomal protein L10) pseudogene, ESTs, STSs and GSSs /FEA=CDS /DB XREF=gi:9795199 /UG=Hs.272340 Human DNA sequence from clone RP11-209A2 on chromosome 6. Contains an RPL10 (60S ribosomal protein L10) pseudogene, ESTs, STSs and GSSs
206120_at	gb:NM_001772.1 /DEF=Homo sapiens CD33 antigen (gp67) (CD33), mRNA. /FEA=mRNA /GEN=CD33 /PROD=CD33 antigen (gp67) /DB XREF=gi:4502654 /UG=Hs.83731 CD33 antigen (gp67) /FL=gb:M23197.1 gb:NM_001772.1
202737_s_at	gb:NM_012321.1 /DEF=Homo sapiens U6 snRNA-associated Sm-like protein (LSM4), mRNA. /FEA=mRNA /GEN=LSM4 /PROD=U6 snRNA-associated Sm-like protein /DB XREF=gi:6912485 /UG=Hs.16719 U6 snRNA-associated Sm-like protein /FL=gb:BC003652.1 gb:AF182290.1 gb:AF117235.1 gb:NM_012321.1 gb:AF251218.1
201416_at	Consensus includes gb:BG528420 /FEA=EST /DB XREF=gi:1351957 /DB XREF=est:602579853EL /CLONE=IMAGE:4719060 /UG=Hs.83484 SRY (sex determining region Y)-box 4 /FL=gb:NM_003107.1
214084_x_at	Consensus includes gb:AW072388 /FEA=EST /DB XREF=gi:6027386 /DB XREF=est:xa07d05.x1 /CLONE=IMAGE:2567625 /UG=Hs.1583
204861_s_at	neutrophil cytosolic factor 1 (47kD, chronic granulomatous disease, autosomal 1) /DB XREF=gi:4758751 /UG=Hs.79019 baculoviral IAP repeat-containing 1 /FL=gb:U19251.1 gb:NM_004536.1
221666_s_at	beat-Containing 1 /DB XREF=gi:4758751 /UG=Hs.79019 baculoviral IAP repeat-containing 1 /FL=gb:U19251.1 gb:NM_004536.1
218421_at	gb:BC004470.1 /DEF=Homo sapiens, clone MGC:10332, mRNA, complete cds. /FEA=mRNA /PROD=Unknown (protein for MGC:10332) /DB XREF=gi:13325315 /UG=Hs.71869 apoptosis-associated speck-like protein containing a CARD /FL=gb:BC004470.1
217794_at	gb:NM_022766.1 /DEF=Homo sapiens hypothetical protein FLJ23239 (FLJ23239), mRNA. /FEA=mRNA /GEN=FLJ23239 /PROD=hypothetical protein FLJ23239 /DB XREF=gi:12232440 /UG=Hs.34516 hypothetical protein FLJ23239 /FL=gb:NM_022766.1 gb:BC004278.1
201558_at	gb:NM_018457.1 /DEF=Homo sapiens DRF2p564J157 protein (DKFZP564J157), mRNA. /FEA=mRNA /GEN=DKFZP564J157 /PROD=DKFZP564J157 protein /DB XREF=gi:8922156 /UG=Hs.63042 DKFZP564J157 protein /FL=gb:AF217517.1 gb:NM_018457.1
218055_s_at	gb:NM_003610.1 /DEF=Homo sapiens RAE1 (RNA export 1, S.pombe) homolog /DB XREF=gi:4506398 /UG=Hs.196209 RAE1 (RNA export 1, S.pombe) homolog /FL=gb:U84720.1 gb:NM_003610.1
202191_s_at	gb:NM_018268.1 /DEF=Homo sapiens hypothetical protein FLJ10904 (FLJ10904), mRNA. /FEA=mRNA /GEN=FLJ10904 /PROD=hypothetical protein FLJ10904 /DB XREF=gi:8922759 /UG=Hs.16470 hypothetical protein FLJ10904 /FL=gb:NM_018268.1
205550_s_at	Consensus includes gb:BE439987 /FEA=EST /DB XREF=gi:9439470 /DB XREF=est:HTM1-745F /UG=Hs.226133 growth arrest-specific 7 /FL=gb:AB007854.1 gb:NM_005890.1
202941_at	gb:NM_004899.1 /DEF=Homo sapiens brain and reproductive organ-expressed (TNFRSF1A modulator) (BRE), mRNA. /FEA=mRNA /GEN=BRE /PROD=brain and reproductive organ-expressed (TNFRSF1A modulator) /FL=gb:BC001251.1 gb:NM_004899.1 gb:L38616.1
217814_at	reproductive organ-expressed (TNFRSF1A modulator) /FL=gb:BC001251.1 gb:NM_004899.1 gb:L38616.1
212051_at	gb:NM_021074.1 /DEF=Homo sapiens NADH dehydrogenase (ubiquinone) flavoprotein 2 (24kD) (NDUFV2), mRNA. /FEA=mRNA /GEN=NDUFV2 /PROD=NADH dehydrogenase (ubiquinone) flavoprotein 2 (24kD) /DB XREF=gi:10835024 /UG=Hs.51299 NADH dehydrogenase (ubiquinone) flavoprotein 2 (24kD) /FL=gb:NM_021074.1 gb:BC001632.1 gb:M22538.1
212386_at	gb:NM_020198.1 /DEF=Homo sapiens GK001 protein (GK001), mRNA. /FEA=mRNA /GEN=GK001 /PROD=GK001 protein /DB XREF=gi:9910241 /UG=Hs.8207 GK001 protein /FL=gb:AF113221.1 gb:BC001300.1 gb:AF226054.1 gb:NM_020198.1
218571_s_at	Consensus includes gb:AA676803 /FEA=EST /DB XREF=gi:2657325 /DB XREF=est:zj65b04.s1 /CLONE=IMAGE:455119 /UG=Hs.13996 Homo sapiens cDNA: FLJ23260 fls. clone COL05804, highly similar to HSU09011 Human clone 23652 mRNA sequence
203462_x_at	Consensus includes gb:BF592782 /FEA=EST /DB XREF=gi:11685106 /DB XREF=est:j94d06.x1 /CLONE=IMAGE:3442594 /UG=Hs.289068 Homo sapiens cDNA FLJ11918 fls. clone HEMBB1000272
218642_s_at	gb:NM_014169.1 /DEF=Homo sapiens HSPC134 protein (HSPC134), mRNA. /FEA=mRNA /GEN=HSPC134 /PROD=HSPC134 protein /DB XREF=gi:7661793 /UG=Hs.279761 HSPC134 protein /FL=gb:AF212243.1 gb:AF161483.1 gb:NM_014169.1
200024_at	gb:NM_003751.1 /DEF=Homo sapiens eukaryotic translation initiation factor 3, subunit 9 (eta, 116kD) (EIF3S9), mRNA. /FEA=mRNA /GEN=EIF3S9 /PROD=eukaryotic translation initiation factor 3, subunit 9 (eta, 116kD) /DB XREF=gi:4503526 /UG=Hs.57783 eukaryotic translation initiation factor 3, subunit 9 (eta, 116kD) /FL=gb:U62583.1 gb:NM_003751.1
218101_s_at	gb:NM_024300.1 /DEF=Homo sapiens hypothetical protein MGC2217 (MGC2217), mRNA. /FEA=mRNA /GEN=MGC2217 /PROD=hypothetical protein MGC2217 /DB XREF=gi:13236525 /UG=Hs.323164 hypothetical protein MGC2217 /FL=gb:BC002546.1 gb:NM_024300.1
	gb:NM_001009.1 /DEF=Homo sapiens ribosomal protein S5 (RP55), mRNA. /FEA=mRNA /GEN=RP55 /PROD=ribosomal protein S5 /DB XREF=gi:4506728 /UG=Hs.76194 ribosomal protein S5 (RP55) /FL=gb:NM_001009.1 gb:U14970.1
	gb:NM_004549.1 /DEF=Homo sapiens NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 2 (14.5kD, B14.5b) (NDUFC2), mRNA. /FEA=mRNA /GEN=NDUFC2 /PROD=NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 2 (14.5kD, B14.5b) /DB XREF=gi:4758783 /UG=Hs.193313 NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 2 (14.5kD, B14.5b) /FL=gb:AF087659.1 gb:AF070652.1 gb:NM_004549.1

203929_x_at	gb:BC000587.1 / DEF=Homo sapiens, clone MGC:2198, mRNA, complete cds. / FEA=mRNA / PROD=Unknown (protein for MGC:2198) / DB_XREF=gi:12653618 / UG=Hs.227152 mannan-binding lectin serine protease 1 (C4C2 activating component of Ra-reactive Factor) / FL=gb:BC000587.1
208454_s_at	gb:NM_016134.1 / DEF=Homo sapiens aminopeptidase (LOC51670), mRNA. / FEA=CDS / GEN=LOC51670 / PROD=aminopeptidase / DB_XREF=gi:7706386 / UG=Hs.278993 aminopeptidase / FL=gb:AF107834.1 gb:NM_016134.1
214351_x_at	Consensus includes gb:AA789278 / FEA=EST / DB_XREF=gi:2849398 / DB_XREF=est:aj28b10.sl / CLONE=1391611 / UG=Hs.180842 ribosomal protein l13
207075_at	gb:NM_004895.1 / DEF=Homo sapiens chromosome 1 open reading frame 7 (C1ORF7), mRNA. / FEA=mRNA / GEN=C1ORF7 / PROD=chromosome 1 open reading frame 7 / DB_XREF=gi:4757727 / UG=Hs.159483 chromosome 1 open reading frame 7 / FL=gb:AF054176.1 gb:NM_004895.1
201449_at	Consensus includes gb:AL567227 / FEA=EST / DB_XREF=gi:12920378 / DB_XREF=est:AL567227 / CLONE=CS0DF027Y11 (3 prime) / UG=Hs.239489 TIA1 cytotoxic granule-associated RNA-binding protein / FL=gb:NM_022037.1 gb:M77142.1
213720_s_at	Consensus includes gb:AI831675 / FEA=EST / DB_XREF=gi:5452346 / DB_XREF=est:wj50q03.xl / CLONE=IMAGE:2406292 / UG=Hs.78202 SWI5NF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4
201593_s_at	Consensus includes gb:AV716798 / FEA=EST / DB_XREF=gi:10813950 / DB_XREF=est:AV716798 / CLONE=DCBRAB02 / UG=Hs.6375 uncharacterized hypothalamus protein HT010 / FL=gb:AF220184.1 gb:NM_018471.1
208095_s_at	gb:NM_001222.1 / DEF=Homo sapiens calmodulin-dependent protein kinase (Cam kinase) II gamma (CMK2G), mRNA. / FEA=mRNA / GEN=CMK2G / PROD=calmodulin-dependent protein kinase (Cam kinase) II gamma / DB_XREF=gi:4502554 / UG=Hs.250857 calmodulin-dependent protein kinase (Cam kinase) II gamma / FL=gb:U81554.1 gb:NM_001222.1
201173_x_at	gb:NM_006600.1 / DEF=Homo sapiens nuclear distribution gene C (A.nidulans) homolog (NUDC), mRNA. / FEA=mRNA / GEN=NUDC / PROD=nuclear distribution gene C (A.nidulans) homolog / DB_XREF=gi:5729952 / UG=Hs.263812 nuclear distribution gene C (A.nidulans) homolog / FL=gb:BC002399.1 gb:BC003132.1 gb:AB019408.1 gb:AF130736.1 gb:AF125465.1 gb:AF100760.1 gb:NM_006600.1
217839_at	gb:NM_006070.1 / DEF=Homo sapiens TRK-fused gene (TFG), mRNA. / FEA=mRNA / GEN=TFG / PROD=TRK-fused gene / DB_XREF=gi:5174718 / UG=Hs.250897 TRK-fused gene / FL=gb:NM_006070.1
203229_s_at	gb:NM_003993.1 / DEF=Homo sapiens CDC-like kinase 2 (CLK2), transcript variant phclik2, mRNA. / FEA=mRNA / GEN=CLK2 / PROD=CDC-like kinase 2 isoform hclik2 / DB_XREF=gi:4502882 / UG=Hs.73986 CDC-like kinase 2 / FL=gb:NM_003993.1 gb:129218.1
203656_at	gb:NM_014845.1 / DEF=Homo sapiens KIAA0274 gene product (KIAA0274), mRNA. / FEA=mRNA / GEN=KIAA0274 / PROD=KIAA0274 gene product / DB_XREF=gi:7662033 / UG=Hs.10037 KIAA0274 gene product / FL=gb:DB7464.1 gb:NM_014845.1
218763_at	gb:NM_016930.1 / DEF=Homo sapiens syntaxin 18 (STX18), mRNA. / FEA=mRNA / GEN=STX18 / PROD=syntaxin 18 / DB_XREF=gi:8394375 / UG=Hs.13406 syntaxin 18 / FL=gb:AB028741.1 gb:NM_016930.1
213846_at	Consensus includes gb:AA382702 / FEA=EST / DB_XREF=gi:2035020 / DB_XREF=est:EST95939 / UG=Hs.3462 cytochrome c oxidase subunit VIIc
201214_s_at	gb:NM_002712.1 / DEF=Homo sapiens protein phosphatase 1, regulatory subunit 7 (PPP1R7), mRNA. / FEA=mRNA / GEN=PPP1R7 / PROD=protein phosphatase 1, regulatory subunit 7 / DB_XREF=gi:4506012 / UG=Hs.36587 protein phosphatase 1, regulatory subunit 7 / FL=gb:BC000910.1 gb:NM_002712.1
216505_x_at	Consensus includes gb:AL118502 / DEF=Human DNA sequence from clone RP11-371119 on chromosome 20 Contains a novel gene, a gene similar to the gene for ribosomal protein S10, ESTs, STSs, and CpG islands / FEA=mRNA_3 / DB_XREF=gi:8894621 / UG=Hs.284299 Human DNA sequence from clone RP11-371119 on chromosome 20 Contains a novel gene, a gene similar to the gene for ribosomal protein S10, ESTs, STSs, and CpG islands
203459_s_at	gb:NM_022575.1 / DEF=Homo sapiens vacuolar protein sorting 16 (yeast homolog) / DB_XREF=gi:12007657 / UG=Hs.302441 vacuolar protein sorting 16 (yeast homolog) / FL=gb:AF308801.1 gb:NM_022575.1
202880_s_at	gb:NM_004762.1 / DEF=Homo sapiens pleckstrin homology, Sec7 and coiledcoil domains 1(cytohesin 1) (PSCD1), transcript variant 1, mRNA. / FEA=mRNA / GEN=PSCD1 / PROD=cytohesin 1, isoform 1 / DB_XREF=gi:4758963 / UG=Hs.1050 pleckstrin homology, Sec7 and coiledcoil domains 1(cytohesin 1) / FL=gb:M85169.1 gb:NM_004762.1 gb:NM_017456.1
43511_s_at	Cluster incl. AI201594:qc02h12.xl Homo sapiens cDNA, 3' end / clone=IMAGE-1708487 / clone_end=3 / gb=AI201594 / gi=3754200 / UG=Hs.239333 / len=591
203519_s_at	gb:NM_015542.1 / DEF=Homo sapiens regulator of nonsense transcripts 2 (DKF2P434D222 protein (RENT2)), mRNA. / FEA=mRNA / GEN=RENT2 / PROD=regulator of nonsense transcripts 2 / DB_XREF=gi:11693131 / UG=Hs.3862 regulator of nonsense transcripts 2; DKF2P434D222 protein / FL=gb:AF301013.1 gb:NM_015542.1 gb:AV013249.1 gb:AF318574.1
206214_at	gb:NM_005084.1 / DEF=Homo sapiens phospholipase A2, group VII (platelet-activating factor acetylhydrolase, plasma) (PLA2G7), mRNA. / FEA=mRNA / GEN=PLA2G7 / PROD=phospholipase A2, group VII (platelet-activating factor acetylhydrolase, plasma) / DB_XREF=gi:4826883 / UG=Hs.93304 phospholipase A2, group VII (platelet-activating factor acetylhydrolase,

	plasma) /FL-gb:U24577.1 gb:NM_005084.1 gb:U20157.1
209933_s_at	gb:AF020314.1 /DEF=Homo sapiens CMRF-35-H9 mRNA, complete cds. /FEA=mrna /PROD=CMRF-35-H9 /DB_XREF=gi:4103065 /UG=Hs.9688 leukocyte membrane antigen /FL-gb:AF020314.1
202105_at	gb:NM_001551.1 /DEF=Homo sapiens immunoglobulin (CD79A) binding protein 1 (IGBP1), mRNA. /FEA=mrna /GEN=IGBP1 /PROD=Immunoglobulin-binding protein 1 /DB_XREF=gi:4557662 /UG=Hs.3631 immunoglobulin (CD79A) binding protein 1 /FL-gb:BC004137.1 gb:NM_001551.1
218138_at	gb:NM_018848.1 /DEF=Homo sapiens McKusick-Kaufman syndrome (MKKS), mRNA. /FEA=mrna /GEN=MKKS /PROD=McKusick-Kaufman syndrome protein /DB_XREF=gi:9055271 /UG=Hs.46743 McKusick-Kaufman syndrome /FL-gb:AF275813.1 gb:AF221992.1
220864_s_at	gb:NM_015965.1 /DEF=Homo sapiens CGI-39 protein; cell death-regulatory protein GRIM19 (LOC51079), mRNA. /FEA=mrna /GEN=LOC51079 /PROD=CGI-39 protein; cell death-regulatory protein GRIM19 /FL-gb:AF132973.1 gb:AF155662.1 gb:NM_015965.1
213355_at	Cell death-regulatory protein GRIM19 /FL-gb:AF132973.1 gb:AF155662.1 gb:NM_015965.1
	Consensus includes gb:AI989567 /FEA=EST /DB_XREF=gi:5836448 /DB_XREF=est:ws34e03.x1 /CLONE=IMAGE:2499100 /UG=Hs.34578
	alpha2,3-sialyltransferase
212587_s_at	Consensus includes gb:AI809341 /FEA=EST /DB_XREF=gi:5395907 /DB_XREF=est:we96c09.x1 /CLONE=IMAGE:2348944 /UG=Hs.170121
	protein tyrosine phosphatase, receptor type, C
205992_s_at	gb:NM_000585.1 /DEF=Homo sapiens interleukin 15 (IL15), mRNA. /FEA=mrna /GEN=IL15 /PROD=interleukin 15 /DB_XREF=gi:10835152 /UG=Hs.168132 interleukin 15 /FL-gb:NM_000585.1 gb:U14407.1
203262_s_at	gb:NM_004699.1 /DEF=Homo sapiens DNA segment on chromosome X (unique) 9928 expressed sequence (DMS9928E), mRNA. /FEA=mrna /GEN=DMS9928E /PROD=XAP-5 protein /DB_XREF=gi:4758219 /UG=Hs.54277 DNA segment on chromosome X (unique) 9928 expressed sequence /FL-gb:BC000028.1 gb:D83260.1 gb:AD001530.1 gb:NM_004699.1
213357_at	Consensus includes gb:AV701318 /FEA=EST /DB_XREF=gi:10717648 /DB_XREF=est:AV701318 /CLONE=ADAAGD10 /UG=Hs.278626 ArgAb1-interacting protein ArgBP2
207628_s_at	gb:NM_017528.1 /DEF=Homo sapiens putative methyltransferase (HAS04442), mRNA. /FEA=mrna /GEN=HAS04442 /PROD=putative methyltransferase /DB_XREF=gi:8923713 /UG=Hs.155020 putative methyltransferase /FL-gb:NM_017528.1
201527_at	gb:NM_004231.1 /DEF=Homo sapiens ATPase, vacuolar, 14 kD (ATP6S14), mRNA. /FEA=mrna /GEN=ATP6S14 /PROD=ATPase, vacuolar, 14 kD /DB_XREF=gi:4757819 /UG=Hs.79089 ATPase, vacuolar, 14 kD /FL-gb:D49400.1 gb:NM_004231.1
202282_at	gb:NM_004493.1 /DEF=Homo sapiens hydroxycyl-Coenzyme A dehydrogenase, type II (HADH2), mRNA. /FEA=mrna /GEN=HADH2 /PROD=hydroxycyl-Coenzyme A dehydrogenase, type II /DB_XREF=gi:4758503 /UG=Hs.171280 hydroxycyl-Coenzyme A dehydrogenase, type II /FL-gb:BC000372.1 gb:BC000829.1 gb:U73514.1 gb:U96132.1 gb:AF035555.1 gb:AF069134.1 gb:NM_004493.1
213735_s_at	Consensus includes gb:AI557312 /FEA=EST /DB_XREF=gi:4489675 /DB_XREF=est:PT2.1_16_E11.r /UG=Hs.1342 cytochrome c oxidase subunit Vb
212472_at	Consensus includes gb:BE965029 /FEA=EST /DB_XREF=gi:11768976 /DB_XREF=est:601658812R1 /CLONE=IMAGE:3886131 /UG=Hs.198793
214805_at	Homo sapiens cDNA: FLJ22463 fis, clone HRC10126
	Consensus includes gb:U79273.1 /DEF=Human clone 23933 mRNA sequence. /FEA=mrna /DB_XREF=gi:1710239 /UG=Hs.239483 Human clone 23933 mRNA sequence
218084_x_at	gb:NM_014164.2 /DEF=Homo sapiens FXID domain-containing ion transport regulator 5 (FXID5), mRNA. /FEA=mrna /GEN=FXID5 /PROD=related to ion channel /DB_XREF=gi:11612664 /UG=Hs.294135 FXID domain-containing ion transport regulator 5 /FL-gb:NM_014164.2 gb:AF161462.1
218204_s_at	gb:NM_024513.1 /DEF=Homo sapiens FYVE and coiled-coil domain containing 1 (FYCOL), mRNA. /FEA=mrna /GEN=FYCOL /PROD=FYVE and coiled-coil domain containing 1 /DB_XREF=gi:13470091 /UG=Hs.257267 FYVE and coiled-coil domain containing 1 /FL-gb:NM_024513.1
200823_x_at	gb:NM_000992.1 /DEF=Homo sapiens ribosomal protein L29 (RPL29), mRNA. /FEA=mrna /GEN=RPL29 /PROD=ribosomal protein L29 /DB_XREF=gi:4506628 /UG=Hs.183698 ribosomal protein L29 /FL-gb:U49083.1 gb:NM_000992.1 gb:U10248.1
208968_s_at	gb:BC002568.1 /DEF=Homo sapiens, hypothetical protein, clone MGC:2478, mRNA, complete cds. /FEA=mrna /PROD=hypothetical protein /DB_XREF=gi:12803484 /UG=Hs.4900 hypothetical protein /FL-gb:AF248964.1 gb:BC002568.1 gb:AF116609.1
208887_at	gb:BC000733.1 /DEF=Homo sapiens, eukaryotic translation initiation factor 3, subunit 4 (delta, 44kD), clone MGC:2053, mRNA, complete cds. /FEA=mrna /PROD=eukaryotic translation initiation factor 3, subunit 4 (delta, 44kD) /DB_XREF=gi:12653882 /UG=Hs.28081 eukaryotic translation initiation factor 3, subunit 4 (delta, 44kD) /FL-gb:AF094850.1 gb:BC000733.1 gb:AF020833.1
214097_at	Consensus includes gb:AW024383 /FEA=EST /DB_XREF=gi:5877913 /DB_XREF=est:ww03e06.x1 /CLONE=IMAGE:2528482 /UG=Hs.1948 ribosomal protein S21

212191_x_at	Consensus includes gb:AW574664 /FEA=EST /DB_XREF=gi:7246203 /DB_XREF=est:UI-HF-BLO-abw-d-10-0-UI.s1 /CLONE=IMAGE:3057859 /UG=Hs.180842 ribosomal protein L13
217957_at	gb:NM_013242.1 /DEF=Homo sapiens similar to mouse Glt3 or D. melanogaster transcription factor IIB (AF093680), mRNA. /FEA=mrna /GEN=AF093680 /PROD=similar to mouse Glt3 or D. melanogaster transcription factor IIB /DB_XREF=gi:8392874 /UG=Hs.279818 similar to mouse Glt3 or D. melanogaster transcription factor IIB /FL=gb:BC005152.1 gb:AF093680.1 gb:NM_013242.1
201658_at	Consensus includes gb:AUI51560 /FEA=EST /DB_XREF=gi:11013081 /DB_XREF=est:AUI51560 /CLONE=NT2RP200555 /UG=Hs.242894 ADP-ribosylation factor-like 1 /FL=gb:NM_001177.2 gb:L28997.1
218123_at	gb:NM_017835.1 /DEF=Homo sapiens chromosome 21 open reading frame 59 (C21ORF59), mRNA. /FEA=mrna /GEN=C21ORF59 /PROD=hypothetical protein FLJ20467 /DB_XREF=gi:8923436 /UG=Hs.5811 chromosome 21 open reading frame 59 /FL=gb:NM_021254.1 gb:BC000709.1 gb:NM_017835.1 gb:AF282851.1
205241_at	gb:NM_005138.1 /DEF=Homo sapiens SCO (cytochrome oxidase deficient, yeast) homolog 2 (SCO2), nuclear gene encoding mitochondrial protein, mRNA. /FEA=mrna /GEN=SCO2 /PROD=SCO (cytochrome oxidase deficient, yeast) homolog 2 /DB_XREF=gi:4826991 /UG=Hs.278431 SCO (cytochrome oxidase deficient, yeast) homolog 2 /FL=gb:NM_005138.1
203740_at	gb:NM_005792.1 /DEF=Homo sapiens M-phase phosphoprotein 6 (MPHSP6), mRNA. /FEA=mrna /GEN=MPHSP6 /PROD=M-phase phosphoprotein 6 /DB_XREF=gi:5031918 /UG=Hs.152720 M-phase phosphoprotein 6 /FL=gb:BC005242.1 gb:NM_005792.1
221263_s_at	gb:NM_031287.1 /DEF=Homo sapiens hypothetical protein MGC3133 (MGC3133), mRNA. /FEA=mrna /GEN=MGC3133 /PROD=hypothetical protein MGC3133 /DB_XREF=gi:13775199 /FL=gb:NM_031287.1
218831_s_at	gb:NM_004107.1 /DEF=Homo sapiens Fc fragment of IgG, receptor, transporter, alpha (FCGRT), mRNA. /FEA=mrna /GEN=FCGRT /PROD=Fc fragment of IgG, receptor, transporter, alpha /DB_XREF=gi:4758345
201400_at	UG=Hs.111903 Fc fragment of IgG, receptor, transporter, alpha /FL=gb:NM_004107.1 gb:U12255.1
203136_at	gb:NM_002795.1 /DEF=Homo sapiens proteasome (prosome, macropain) subunit, beta type, 3 (PSMB3), mRNA. /FEA=mrna /GEN=PSMB3 /PROD=proteasome (prosome, macropain) subunit, beta type, 3 /DB_XREF=gi:4506196
203136_at	UG=Hs.82793 proteasome (prosome, macropain) subunit, beta type, 3 /FL=gb:NM_002795.1 gb:D26598.1
203136_at	gb:NM_006423.1 /DEF=Homo sapiens Rab acceptor 1 (prenylated) (RABAC1), mRNA. /FEA=mrna /GEN=RABAC1 /PROD=Rab acceptor 1 (prenylated) /DB_XREF=gi:5453959 /UG=Hs.11417 Rab acceptor 1 (prenylated) /FL=gb:NM_006423.1 gb:AF112202.1
205382_s_at	gb:NM_001928.1 /DEF=Homo sapiens D component of complement (adipsin) (DF), mRNA. /FEA=mrna /GEN=DF /PROD=adipsin complement factor D precursor /DB_XREF=gi:4503308 /UG=Hs.155597 D component of complement (adipsin) /FL=gb:M84526.1 gb:NM_001928.1
208714_at	gb:AF092131.1 /DEF=Homo sapiens 51kDa subunit of NADH dehydrogenase mRNA, complete cds. /FEA=mrna /PROD=51kDa subunit of NADH dehydrogenase /DB_XREF=gi:5138911 /UG=Hs.7744 NADH dehydrogenase (ubiquinone) flavoprotein 1 (51kD) /FL=gb:AF053070.1 gb:AF092131.1 gb:NM_007103.1
209224_s_at	gb:BC003674.1 /DEF=Homo sapiens, NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2 (8kD, B8), clone MGC:12315, mRNA, complete cds. /FEA=mrna /PROD=NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2 (8kD, B8) /DB_XREF=gi:13277539 /UG=Hs.163867 NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2 (8kD, B8) /FL=gb:BC003674.1 gb:AF047185.1 gb:NM_002488.1 gb:AF077029.1
210574_s_at	gb:AF241788.1 /DEF=Homo sapiens NPD011 (NPD011) mRNA, complete cds. /FEA=mrna /GEN=NPD011 /PROD=NPD011 /DB_XREF=gi:12005492 /UG=Hs.263812 nuclear distribution gene C (A.nidulans) homolog /FL=gb:AF241788.1
214259_s_at	Consensus includes gb:A1144075 /FEA=EST /DB_XREF=gi:3665884 /DB_XREF=est:q163e12.x1 /CLONE=IMAGE:1861198
209234_at	UG=Hs.6980 aldo-keto reductase family 7, member A2 (aflatoxin aldehyde reductase)
209234_at	Consensus includes gb:BF939474 /FEA=EST /DB_XREF=gi:12356794 /DB_XREF=est:nac76d12.x1 /CLONE=IMAGE:3440303 /UG=Hs.129908 KIAA0591 protein /FL=gb:BC001415.1
203654_s_at	gb:NM_004645.1 /DEF=Homo sapiens collagen (COL1), mRNA. /FEA=mrna /GEN=COL1 /PROD=collin /DB_XREF=gi:4758023 /UG=Hs.966 collin /FL=gb:U06632.1 gb:NM_004645.1
201129_at	gb:NM_006276.2 /DEF=Homo sapiens splicing factor, arginineserine-rich 7 (35kD) (SFRS7), mRNA. /FEA=mrna /GEN=SFRS7 /PROD=splicing factor, arginineserine-rich 7 (35kD) /DB_XREF=gi:6857827 /UG=Hs.184167 splicing factor, arginineserine-rich 7 (35kD) /FL=gb:BC000997.2 gb:L22253.1 gb:NM_006276.2
202451_at	gb:BC000365.1 /DEF=Homo sapiens, general transcription factor IIF, polypeptide 1 (62kD subunit), clone MGC:8323, mRNA, complete cds. /FEA=mrna /PROD=general transcription factor IIF, polypeptide 1 (62kD subunit) /DB_XREF=gi:12653194 /UG=Hs.89578 general transcription factor IIF, polypeptide 1 (62kD subunit)
218072_at	gb:NM_014186.1 /DEF=Homo sapiens HSPC166 protein (HSPC166), mRNA. /FEA=mrna /GEN=HSPC166 /PROD=HSPC166 protein /DB_XREF=gi:7661827 /UG=Hs.279836 HSPC166 protein /FL=gb:ALJ136688.1 gb:AF161515.1 gb:NM_014186.1

203063_at	gb:NM_014634.1 /DEF=Homo sapiens KIAA0015 gene product (KIAA0015), mRNA. /FEA=mRNA /GEN=KIAA0015 /PROD=KIAA0015 gene product /DB_XREF=gi:7661861 /UG=Hs.278441 KIAA0015 gene product /FL=gb:D13640.1 gb:NM_014634.1
204037_at	Consensus includes gb:BF055366 /FEA=EST /DB_XREF=gi:10809262 /DB_XREF=est:777810.x1 /CLONE=IMAGE:3392587 /UG=Hs.75794 endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 2 /FL=gb:U78192.1 gb:U80811.1 gb:NM_001401.1
218298_s_at	gb:NM_024952.1 /DEF=Homo sapiens hypothetical protein FLJ20950 (FLJ20950), mRNA. /FEA=mRNA /GEN=FLJ20950 /PROD=hypothetical protein FLJ20950 /DB_XREF=gi:13376436 /UG=Hs.285673 hypothetical protein FLJ20950 /FL=gb:NM_024952.1
204158_s_at	gb:NM_006019.1 /DEF=Homo sapiens T-cell, immune regulator 1 (TCIRGL), mRNA. /FEA=mRNA /GEN=TCIRGL /PROD=ATPase, H+ transporting, 116kD /DB_XREF=gi:5174620 /UG=Hs.46465 T-cell, immune regulator 1 /FL=gb:U45285.1 gb:NM_006019.1
208842_s_at	Consensus includes gb:W93787 /FEA=EST /DB_XREF=gi:1422930 /DB_XREF=est:zd96c09.s1 /CLONE=IMAGE:357328 /UG=Hs.6880 DKFZP434D156 protein /FL=gb:BC001408.1
203047_at	gb:NM_005990.1 /DEF=Homo sapiens serine/threonine kinase 10 (STK10), mRNA. /FEA=mRNA /GEN=STK10 /PROD=serine/threonine kinase 10 /DB_XREF=gi:5174700 /UG=Hs.16134 serine/threonine kinase 10 /FL=gb:AB015718.1 gb:NM_005990.1 gb:AF119894.1
213408_s_at	Consensus includes gb:AK024034.1 /DEF=Homo sapiens cDNA FLJ13972 fis, clone Y79AA1001548, highly similar to PHOSPHATIDYLINOSITOL 4-KINASE ALPHA (BC 2.7.1.1.67). /FEA=mRNA /DB_XREF=gi:10436297 /UG=Hs.171625 phosphatidylinositol 4-kinase, catalytic, alpha polypeptide
209858_x_at	gb:BC002877.1 /DEF=Homo sapiens, similar to hypothetical protein FLJ11585, clone MGC:11258, mRNA, complete cds. /FEA=mRNA /PROD=Similar to hypothetical protein FLJ11585 /DB_XREF=gi:12804048 /UG=Hs.315367 Homo sapiens, similar to hypothetical protein FLJ11585, clone MGC:11258, mRNA, complete cds /FL=gb:BC002877.1
35626_at	Cluster Incl. U30894:Human N-sulphoglucosamine sulphonylhydrolase mRNA, complete cds /cds=(12,1520) /gb=U30894 /gi=1173542 /ug=Hs.31074 /len=2657
201871_s_at	gb:NM_015853.1 /DEF=Homo sapiens ORF (LOC51035), mRNA. /FEA=mRNA /GEN=LOC51035 /PROD=unknown protein LOC51035 /DB_XREF=gi:7705653 /UG=Hs.77868 ORF /FL=gb:BC000902.1 gb:M68864.1 gb:NM_015853.1
212204_at	Consensus includes gb:AL049944.1 /DEF=Homo sapiens mRNA; cDNA DKFZp564G2022 (from clone DKFZp564G2022); partial cds. /FEA=mRNA /GEN=DKFZp564G2022 /PROD=hypothetical protein /DB_XREF=gi:4884189 /UG=Hs.16492 DKFZp564G2022 protein
217802_s_at	gb:NM_022731.1 /DEF=Homo sapiens similar to rat nuclear ubiquitously casein kinase 2 (NUCKS), mRNA. /FEA=mRNA /GEN=NUCKS /PROD=similar to rat nuclear ubiquitously casein kinase 2 /DB_XREF=gi:12232386 /UG=Hs.118064 similar to rat nuclear ubiquitously casein kinase 2 /FL=gb:NM_022731.1 gb:BC000805.1
201960_s_at	gb:NM_015057.1 /DEF=Homo sapiens KIAA0916 protein (KIAA0916), mRNA. /FEA=mRNA /GEN=KIAA0916 protein /DB_XREF=gi:7662379 /UG=Hs.151411 KIAA0916 protein /FL=gb:AF075587.1 gb:AF083244.1 gb:NM_015057.1
47608_at	Cluster Incl. AF697401:tg18h09.x1 Homo sapiens cDNA, 3' end /clone=IMAGE-2209217 /clone_end=3 /gb=AF697401 /gi=4985301 /ug=Hs.9741 /len=639
210250_x_at	gb:AF067854.1 /DEF=Homo sapiens adenylosuccinate lyase (ADSL) mRNA, alternatively spliced, complete cds. /FEA=mRNA /GEN=ADSL /PROD=adenylosuccinate lyase /DB_XREF=gi:3211983 /UG=Hs.75527 adenylosuccinate lyase /FL=gb:AF067854.1
218495_at	gb:NM_004182.1 /DEF=Homo sapiens ubiquitously-expressed transcript (UXT), mRNA. /FEA=mRNA /GEN=UXT /PROD=ubiquitously-expressed transcript /DB_XREF=gi:4759297 /UG=Hs.172791 ubiquitously-expressed transcript /FL=gb:BC000720.1 gb:AF092737.1 gb:NM_004182.1 gb:AF083244.1 gb:AF083242.1
201106_at	gb:NM_002085.1 /DEF=Homo sapiens glutathione peroxidase 4 (phospholipid hydroperoxidase) (GPX4), mRNA. /FEA=mRNA /GEN=GPX4 /PROD=glutathione peroxidase 4 /DB_XREF=gi:4504106 /UG=Hs.2706 glutathione peroxidase 4 (phospholipid hydroperoxidase) /FL=gb:NM_002085.1
203569_s_at	gb:NM_003611.1 /DEF=Homo sapiens chromosome X open reading frame 5 (CXORF5), mRNA. /FEA=mRNA /GEN=CXORF5 /PROD=chromosome X open reading frame 5 /DB_XREF=gi:4503178 /UG=Hs.6483 oral-facial-digital syndrome 1 gene /FL=gb:NM_003611.1
201316_at	Consensus includes gb:AL523904 /FEA=EST /DB_XREF=gi:12787397 /DB_XREF=est:AL523904 /CLONE=CS0DC003YB07 (3 prime) /UG=Hs.181309 proteasome [prosome, macropain] subunit, alpha type, 2 /FL=gb:NM_002787.1
218336_at	gb:NM_012394.2 /DEF=Homo sapiens prefoldin 2 (PFND2), mRNA. /FEA=mRNA /GEN=PFND2 /PROD=prefoldin 2 /DB_XREF=gi:12408674 /UG=Hs.298229 prefoldin 2 /FL=gb:NM_012394.2 gb:AF165883.1 gb:AF117237.1 gb:AF151065.1
209370_s_at	Consensus includes gb:BE502377 /FEA=EST /DB_XREF=gi:9704785 /DB_XREF=est:hv22g03.x1 /CLONE=IMAGE:3198100 /UG=Hs.167679 SH3-domain binding protein 2 /FL=gb:AB000462.1 gb:AF000936.1
201036_s_at	gb:NM_005327.1 /DEF=Homo sapiens L-3-hydroxyacyl-Coenzyme A dehydrogenase, short chain (HADHSC), mRNA. /FEA=mRNA /GEN=HADHSC /PROD=L-3-hydroxyacyl-Coenzyme A dehydrogenase, short chain /DB_XREF=gi:4885386 /UG=Hs.8110 L-3-hydroxyacyl-Coenzyme A dehydrogenase, short chain /FL=gb:BC000306.1 gb:NM_005327.1
208776_at	Consensus includes gb:BF432873 /FEA=EST /DB_XREF=gi:11445036 /DB_XREF=est:7n28a02.x1 /CLONE=IMAGE:3565730 /UG=Hs.90744 proteasome

	(prosoma, macropain) 26S subunit, non-ATPase, 11 / FL=gb:BC000437.1 gb:BC004430.1 gb:AB003102.1 gb:AF001212.1 gb:NM_002815.1
214765_s_at	Consensus includes gb:AK024677.1 /DEF=Homo sapiens cDNA: FLJ21024 fis, clone CAE06651, highly similar to HUMPT Human LTR mRNA. / FEA=mrna /DB XREF=gi:10437016 /UG=Hs.264330 N-acylphosphatase amidohydrolase (acid ceramidase)-like
204225_at	gb:NM_006037.2 /DEF=Homo sapiens histone deacetylase 4 (HDAC4), mRNA. /FEA=mrna /GEN=HDAC4 /PROD=histone deacetylase 4 / DB XREF=gi:13259519 /UG=Hs.91400 histone deacetylase 4 / FL=gb:NM_006037.2 gb:AF132607.1
214170_x_at	Consensus includes gb:AA669797 /FEA=EST /DB XREF=gi:2631296 /DB XREF=est:ag36c01.s1 /CLONE=IMAGE:1118880 /UG=Hs.75653 fumarate hydratase
218210_at	gb:NM_024619.1 /DEF=Homo sapiens hypothetical protein FLJ12171 (FLJ12171), mRNA. /FEA=mrna /GEN=FLJ12171 /PROD=hypothetical protein FLJ12171 /DB XREF=gi:13375839 /UG=Hs.31431 hypothetical protein FLJ12171 /FEA=gb:AL1136631.1 gb:NM_024619.1
218652_s_at	gb:NM_017733.1 /DEF=Homo sapiens hypothetical protein FLJ20265 (FLJ20265), mRNA. /FEA=mrna /GEN=FLJ20265 /PROD=hypothetical protein FLJ20265 /DB XREF=gi:8923239 /UG=Hs.7099 hypothetical protein FLJ20265 /FL=gb:BC001249.1 gb:BC000937.2 gb:NM_017733.1
201270_x_at	gb:NM_015332.1 /DEF=Homo sapiens KIAA1068 protein (KIAA1068), mRNA. /FEA=mrna /GEN=KIAA1068 /PROD=KIAA1068 protein / DB XREF=gi:13357209 /UG=Hs.4770 KIAA1068 protein /FL=gb:BC003691.1 gb:NM_015332.1
203906_at	Consensus includes gb:AI652645 /FEA=EST /DB XREF=gi:4736624 /DB XREF=est:wb30b07.x1 /CLONE=IMAGE:2307157 /UG=Hs.4764 KIAA0763 gene product /FL=gb:AB018306.1 gb:NM_014869.1
221516_s_at	gb:BC002587.1 /DEF=Homo sapiens, clone MGC:1067, mRNA, complete cds. /FEA=mrna /PROD=hypothetical protein / DB XREF=gi:12803520 /UG=Hs.83869 hypothetical protein /FL=gb:BC002587.1
209492_x_at	gb:BC003679.1 /DEF=Homo sapiens, ATP synthase, H+ transporting, mitochondrial F0 complex, subunit e, clone MGC:12532, mRNA, complete cds. /FEA=mrna /PROD=ATP synthase, H+ transporting, mitochondrial F0 complex, subunit e /DB XREF=gi:13277943 / UG=Hs.85539 ATP synthase, H+ transporting, mitochondrial F0 complex, subunit e /FL=gb:BC003679.1
212048_s_at	Consensus includes gb:AW245400 /FEA=EST /DB XREF=gi:6588393 /DB XREF=est:2822751.3prime /CLONE=IMAGE:2822751 /UG=Hs.239307 tyrosyl-tRNA synthetase
204214_s_at	gb:NM_006834.1 /DEF=Homo sapiens RAB32, member RAS oncogene family (RAB32), mRNA. /FEA=mrna /GEN=RAB32 /PROD=RAB32, member RAS oncogene family /DB XREF=gi:5803132 /UG=Hs.32217 RAB32, member RAS oncogene family /FL=gb:U71127.1 gb:NM_006834.1
217796_s_at	gb:NM_017921.1 /DEF=Homo sapiens hypothetical protein FLJ20657 (FLJ20657), mRNA. /FEA=mrna /GEN=FLJ20657 /PROD=hypothetical protein FLJ20657 /DB XREF=gi:89232608 /UG=Hs.164256 hypothetical protein FLJ20657 /FL=gb:NM_017921.1
203327_at	Consensus includes gb:N22903 /FEA=EST /DB XREF=gi:1137053 /DB XREF=est:yx66e04.s1 /CLONE=IMAGE:266718 /UG=Hs.1508 insulin-degrading enzyme /FL=gb:M21188.1 gb:NM_004969.1
208659_at	gb:AF034607.1 /DEF=Homo sapiens chloride channel ABP mRNA, complete cds. /FEA=mrna /PROD=chloride channel ABP /DB XREF=gi:4426566 / UG=Hs.74276 chloride intracellular channel 1 /FL=gb:U93205.1 gb:AF034607.1 gb:AF109197.1 gb:NM_001288.2
222218_s_at	Consensus includes gb:AJ400843.1 /DEF=Homo sapiens partial mRNA for immunoglobulin-like cell surface receptor FDF03-M14, soluble alternative form. /FEA=mrna /GEN=FDF03-M14 /PROD=cell surface receptor FDF03-M14 /DB XREF=gi:9715838 /UG=Hs.122591 paired immunoglobulin-like receptor alpha
211862_x_at	gb:AF015451.1 /DEF=Homo sapiens Usurpin-beta mRNA, complete cds. /FEA=CDS /PROD=Usurpin-beta /DB XREF=gi:3133282 /UG=Hs.195175 CASP8 and FADD-like apoptosis regulator /FL=gb:AF015451.1
209080_x_at	gb:AF118652.1 /DEF=Homo sapiens PKCq-interacting protein PICOT (PICOT) mRNA, complete cds. /FEA=mrna /GEN=PKCq /PROD=PKCq-interacting protein PICOT /DB XREF=gi:6840952 /UG=Hs.42644 thiodoxin-like /FL=gb:BC005289.1 gb:AF118649.1 gb:AF118652.1
200789_at	gb:NM_001398.1 /DEF=Homo sapiens enoyl Coenzyme A hydratase 1, peroxisomal (ECH1), mRNA. /FEA=mrna /GEN=ECH1 /PROD=peroxisomal enoyl-coenzyme A hydratase-like protein /DB XREF=gi:4503446 /UG=Hs.196176 enoyl Coenzyme A hydratase 1, peroxisomal / FL=gb:NM_001398.1 gb:U16660.1
90610_at	Cluster Incl. AI654857:wb65b10.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2310523 /clone_end=3 /gb=AI654857 /gi=4738836 / UG=Hs.160115 /len=621
201704_at	gb:NM_001247.1 /DEF=Homo sapiens ectonucleoside triphosphate diphosphohydrolase 6 (putative function) (ENTPD6), mRNA. / FEA=mrna /GEN=ENTPD6 /PROD=ectonucleoside triphosphate diphosphohydrolase 6 (putative function) /DB XREF=gi:4557422 / UG=Hs.12330 ectonucleoside triphosphate diphosphohydrolase 6 (putative function) /FL=gb:AF039916.1 gb:NM_001247.1
218026_at	gb:NM_014019.1 /DEF=Homo sapiens HSPC009 protein (HSPC009), mRNA. /FEA=mrna /GEN=HSPC009 /PROD=HSPC009 protein / DB XREF=gi:7661731 /UG=Hs.16059 HSPC009 protein /FL=gb:BC002698.1 gb:AF070665.1 gb:NM_014019.1
214771_x_at	Consensus includes gb:AK025604.1 /DEF=Homo sapiens cDNA: FLJ21951 fis, clone HEP04968. /FEA=mrna /DB XREF=gi:10438172 / UG=Hs.84883 KIAA0864 protein
208760_at	Consensus includes gb:AL031714 /DEF=Human DNA sequence from clone LA16-358B7 on chromosome 16 Contains the UBE21 gene for ubiquitin-conjugating enzyme E21 (homologous to yeast UBC9), and an RP520 (40S Ribosomal protein S20) pseudogene. Contains ESTs, STSSs, GSSs and a putative CpG is... /FEA=mrna /DB XREF=gi:4775608 /UG=Hs.84285 ubiquitin-conjugating enzyme E21 (homologous to

	yeast UBC9) /FL=gb:U45328.1 gb:U31933.1 gb:BC000427.1 gb:BC004429.1 gb:U31882.1 gb:U66818.1 gb:U66867.1 gb:U38785.1 gb:NM_003345.1 gb:U29092.1
212607_at	Consensus includes gb:N32526 /FEA=EST /DB_XREF=gi:1152925 /DB_XREF=est:yy1lf04.s1 /CLONE=IMAGE:270943 /UG=Hs.300642 serologically defined colon cancer antigen 8
64418_at	Cluster Incl. A1472320:tbj87c02.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2148482 /clone_end=3 /gb=AI472320 /gi=4334410 /ug=Hs.48504 /len=548
205819_at	gb:NM_006770.1 /DEF=Homo sapiens macrophage receptor with collagenous structure (MARCO), mRNA. /FEA=mrna /GEN=MARCO /PROD=macrophage receptor with collagenous structure /DB_XREF=gi:5803079 /UG=Hs.67726 macrophage receptor with collagenous structure /FL=gb:AF035819.1 gb:NM_006770.1
218019_s_at	gb:NM_021941.1 /DEF=Homo sapiens hypothetical protein FLJ21324 (FLJ21324), mRNA. /FEA=mrna /GEN=FLJ21324 /PROD=hypothetical protein FLJ21324 /DB_XREF=gi:11345479 /UG=Hs.4746 hypothetical protein FLJ21324 /FL=gb:NM_021941.1 gb:BC003651.1
219220_x_at	gb:NM_020191.1 /DEF=Homo sapiens GK002 protein (GK002), mRNA. /FEA=mrna /GEN=GK002 /PROD=GK002 protein /DB_XREF=gi:9910243 /UG=Hs.107127 GK002 protein; gbt protein; chromosome 3 open reading frame 5 /FL=gb:AF321613.1 gb:AF226045.1 gb:NM_020191.1
212355_at	Consensus includes gb:A1075450 /FEA=EST /DB_XREF=gi:3399805 /DB_XREF=est:oz82g10.x1 /CLONE=IMAGE:1681890 /UG=Hs.7911 KIAA0323 protein
214735_at	Consensus includes gb:AW166711 /FEA=EST /DB_XREF=gi:6398236 /DB_XREF=est:yg27h02.x1 /CLONE=IMAGE:2628819 /UG=Hs.185140 KIAA0403 protein
219041_s_at	gb:NM_014374.1 /DEF=Homo sapiens zinc finger protein (AP4), mRNA. /FEA=mrna /GEN=AP4 /PROD=zinc finger protein /DB_XREF=gi:7656889 /UG=Hs.90693 zinc finger protein /FL=gb:BC000363.1 gb:NM_014374.1
209110_s_at	gb:AL050259.1 /DEF=Homo sapiens mRNA; cDNA DKFp564D0782 (from clone DKFp564D0782); complete cds. /FEA=mrna /GEN=DKFp564D0782 /PROD=hypothetical protein /DB_XREF=gi:4886476 /UG=Hs.170160 RAB2, member RAS oncogene family-like /FL=gb:D85757.1 gb:NM_004761.1 gb:AL050259.1
215691_x_at	Consensus includes gb:AV702994 /FEA=EST /DB_XREF=gi:10719324 /DB_XREF=est:AV702994 /CLONE=ADBPB06 /UG=Hs.46967 HSPC034 protein
207614_s_at	gb:NM_003592.1 /DEF=Homo sapiens cullin 1 (CUL1), mRNA. /FEA=mrna /GEN=CUL1 /PROD=cullin 1 /DB_XREF=gi:4503160 /UG=Hs.14541 cullin 1 /FL=gb:U58087.1 gb:NM_003592.1
213405_at	Consensus includes gb:N95443 /FEA=EST /DB_XREF=gi:1267753 /DB_XREF=est:zb81cl2.s1 /CLONE=IMAGE:310006 /UG=Hs.19180 Homo sapiens mRNA; cDNA DKFp564E122 (from clone DKFp564E122)
208835_s_at	Consensus includes gb:AW089673 /FEA=EST /DB_XREF=gi:6047017 /DB_XREF=est:xd21h11.x1 /CLONE=IMAGE:2594469 /UG=Hs.3688 cisplatin resistance-associated overexpressed protein /FL=gb:AB034205.1
202225_at	Consensus includes gb:AW612311 /FEA=EST /DB_XREF=gi:7317497 /DB_XREF=est:hg95e07.x1 /CLONE=IMAGE:2953380 /UG=Hs.306088 v-crk avian sarcoma virus CT10 oncogene homolog /FL=gb:D10656.1 gb:NM_016823.1
218358_at	gb:NM_024324.1 /DEF=Homo sapiens hypothetical protein MGCL1256 (MGCL1256), mRNA. /FEA=mrna /GEN=MGCL1256 /PROD=hypothetical protein MGCL1256 /DB_XREF=gi:13236568 /UG=Hs.28029 hypothetical protein MGCL1256 /FL=gb:BC002894.1 gb:NM_024324.1
213511_s_at	Consensus includes gb:AI167164 /FEA=EST /DB_XREF=gi:3700334 /DB_XREF=est:oo08c10.x1 /CLONE=IMAGE:1565586 /UG=Hs.23200 myotubularin related protein 1
218133_s_at	gb:NM_021824.1 /DEF=Homo sapiens NIF3 (Ngg1 interacting factor 3, S.pombe homolog)-like 1 (NIF3L1), mRNA. /FEA=mrna /GEN=NIF3L1 /PROD=NIF3 (Ngg1 interacting factor 3, S.pombe homolog)-like 1 /DB_XREF=gi:11141898 /UG=Hs.21943 NIF3 (Ngg1 interacting factor 3, S.pombe homolog)-like 1 /FL=gb:AF182416.1 gb:NM_021824.1 gb:AF060513.1 gb:AB038949.1
212007_at	Consensus includes gb:AI927512 /FEA=EST /DB_XREF=gi:5663476 /DB_XREF=est:wo90g11.x1 /CLONE=IMAGE:2462660 /UG=Hs.77495 UBX domain-containing 1
204690_at	gb:NM_004853.1 /DEF=Homo sapiens syntaxin 8 (STX8), mRNA. /FEA=mrna /GEN=STX8 /PROD=syntaxin 8 /DB_XREF=gi:4759187 /UG=Hs.119525 syntaxin 8 /FL=gb:AF062077.1 gb:AF036715.1 gb:AF115323.1 gb:NM_004853.1
210042_s_at	gb:AF073890.1 /DEF=Homo sapiens cathepsin X precursor, mRNA, complete cds. /FEA=mrna /PROD=cathepsin X precursor /DB_XREF=gi:3650497 /UG=Hs.252549 cathepsin X precursor, mRNA, complete cds. /FL=gb:AF032906.1 gb:AF073890.1 gb:NM_001336.1 gb:AF136273.1
32091_at	Cluster Incl. AB007915: Homo sapiens mRNA for KIAA0446 protein, complete cds /cds=(3531,4286) /gb=AB007915 /gi=3413853 /ug=Hs.158286 /len=6944
201135_at	gb:NM_004092.2 /DEF=Homo sapiens enoyl Coenzyme A hydratase, short chain, 1, mitochondrial (ECHS1), nuclear gene encoding mitochondrial protein, mRNA. /FEA=mrna /GEN=ECHS1 /PROD=mitochondrial short-chain enoyl-coenzyme A hydratase 1 precursor /DB_XREF=gi:12707569 /UG=Hs.76394 enoyl Coenzyme A hydratase, short chain, 1, mitochondrial /FL=gb:NM_004092.2 gb:D13900.1
220526_s_at	gb:NM_017971.1 /DEF=Homo sapiens hypothetical protein FLJ10024 (FLJ10024), mRNA. /FEA=mrna /GEN=FLJ10024 /PROD=hypothetical protein FLJ10024 /DB_XREF=gi:8922189 /UG=Hs.182698 hypothetical protein FLJ10024 /FL=gb:NM_017971.1

202531_at	gb:NM_002198.1 / DEF=Homo sapiens interferon regulatory factor 1 (IRF1), mRNA. / FEA=mrna / GEN=IRF1 / PROD=interferon regulatory factor 1 / DB XREF=gi:4504720 / UG=Hs.80645 interferon regulatory factor 1 / FL=gb:NM_002198.1
213465_s_at	Consensus includes gb:BF178769 / FEA=EST / DB XREF=gi:12019514 / DB XREF=est:KGS72 / CLONE=S90413.NIH-107-R.ab1 / UG=Hs.36587 protein phosphatase 1, regulatory subunit 7
202025_x_at	gb:NM_001607.2 / DEF=Homo sapiens acetyl-Coenzyme A acyltransferase 1 (peroxisomal 3-oxoacyl-Coenzyme A thiolase) (ACAA1), nuclear gene encoding mitochondrial protein, mRNA. / FEA=mrna / GEN=ACAA1 / PROD=acetyl-Coenzyme A acyltransferase 1 / DB XREF=gi:6598316 / UG=Hs.166160 acetyl-Coenzyme A acyltransferase 1 (peroxisomal 3-oxoacyl-Coenzyme A thiolase) / FL=gb:BC000635.1 gb:NM_001607.2
203944_x_at	gb:NM_007049.1 / DEF=Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA. / FEA=mrna / GEN=BTN2A1 / PROD=butyrophilin, subfamily 2, member A1 / DB XREF=gi:5921460 / UG=Hs.16963 butyrophilin, subfamily 2, member A1 / FL=gb:U90543.1 gb:NM_007049.1
214290_s_at	Consensus includes gb:AI313324 / FEA=EST / DB XREF=gi:4018929 / DB XREF=est:ta7f02.x2 / CLONE=IMAGE:2050107 / UG=Hs.795 H2A histone family, member O
208415_x_at	gb:NM_005537.1 / DEF=Homo sapiens inhibitor of growth 1 family, member 1 (ING1), mRNA. / FEA=mrna / GEN=ING1 / PROD=inhibitor of growth 1 family, member 1 / DB XREF=gi:5031792 / UG=Hs.46700 inhibitor of growth 1 family, member 1 / FL=gb:AF001954.1 gb:NM_005537.1
216396_s_at	Consensus includes gb:AF131850.1 / DEF=Homo sapiens clone 24988 mRNA sequence. / FEA=mrna / DB XREF=gi:4406694 / UG=Hs.286027 etoposide-induced mRNA
203033_x_at	gb:NM_000143.1 / DEF=Homo sapiens fumarate hydratase (FH), mRNA. / FEA=mrna / GEN=FH / PROD=fumarate hydratase / DB XREF=gi:4503716 / UG=Hs.75653 fumarate hydratase / FL=gb:BC003108.1 gb:M15502.1 gb:U59309.1 gb:U48857.1 gb:NM_000143.1
203971_at	gb:NM_001859.1 / DEF=Homo sapiens solute carrier family 31 (copper transporters), member 1 (SLC31A1), mRNA. / FEA=mrna / GEN=SLC31A1 / PROD=solute carrier family 31 (copper transporters), member 1 / DB XREF=gi:4507014 / UG=Hs.73614 solute carrier family 31 (copper transporters), member 1 / FL=gb:U83460.1 gb:NM_001859.1
203241_at	gb:NM_003369.1 / DEF=Homo sapiens UV radiation resistance associated gene (UVRAG), mRNA. / FEA=mrna / GEN=UVRAG / PROD=UV radiation resistance associated gene / DB XREF=gi:4507860 / UG=Hs.13137 UV radiation resistance associated gene / FL=gb:NM_003369.1 gb:AB012958.1
201142_at	Consensus includes gb:AA577698 / FEA=EST / DB XREF=gi:2355882 / DB XREF=est:nm22h05.s1 / CLONE=IMAGE:1084665 / UG=Hs.151777 eukaryotic translation initiation factor 2, subunit 1 (alpha, 35kD) / FL=gb:BC002513.1 gb:J02645.1 gb:NM_004094.1
208818_s_at	gb:BC000419.1 / DEF=Homo sapiens, catechol-O-methyltransferase, clone MGC:8663, mRNA, complete cds. / FEA=mrna / PROD=catechol-O-methyltransferase / DB XREF=gi:12653300 / UG=Hs.240013 catechol-O-methyltransferase / FL=gb:BC000419.1 gb:M59525.1
203436_at	gb:M65212.1 gb:NM_007310.1 gb:NM_000734.2
201380_at	gb:NM_006413.1 / DEF=Homo sapiens ribonuclease P (30kD) (RPP30), mRNA. / FEA=mrna / GEN=RPP30 / PROD=ribonuclease P (30kD) / DB XREF=gi:5454023 / UG=Hs.139120 ribonuclease P (30kD) / FL=gb:U77665.1 gb:NM_006413.1
203614_at	gb:NM_006371.1 / DEF=Homo sapiens cartilage associated protein (CRTAP), mRNA. / FEA=mrna / GEN=CRTAP / PROD=cartilage associated protein / DB XREF=gi:5453600 / UG=Hs.155481 cartilage associated protein / FL=gb:NM_006371.1
208649_s_at	gb:NM_021645.1 / DEF=Homo sapiens KIAA0266 gene product (KIAA0266), mRNA. / FEA=mrna / GEN=KIAA0266 / PROD=KIAA0266 gene product / DB XREF=gi:11063982 / UG=Hs.127376 KIAA0266 gene product / FL=gb:NM_021645.1 gb:D87455.1
209012_at	gb:AF100752.1 / DEF=Homo sapiens transitional endoplasmic reticulum ATPase mRNA, complete cds. / FEA=mrna / PROD=transitional endoplasmic reticulum ATPase / DB XREF=gi:5410289 / UG=Hs.106357 valosin-containing protein / FL=gb:AF100752.1 gb:NM_007126.2
212100_s_at	Consensus includes gb:AV718192 / FEA=EST / DB XREF=gi:10815344 / DB XREF=est:AV718192 / CLONE=FHTABE08 / UG=Hs.171957 triple functional domain (PTPRF interacting) / FL=gb:AF091395.1
208756_at	Consensus includes gb:293241 / DEF=human DNA sequence from clone 222E13 on chromosome 22. Contains three novel genes, an ATP Synthase G Chain, Mitochondrial (EC 3.6.1.34) pseudogene and the DIAL gene for diaphorase (NADH) (cytochrome b-5 reductase) (EC 1.6.2.2). Contains ESTs, STSs, ... / FEA=mrna 5 / DB XREF=gi:4826450 / UG=Hs.278314 hypothetical protein
213034_at	gb:U36764.1 / DEF=human TGF-beta receptor interacting protein 1 mRNA, complete cds. / FEA=mrna / PROD=TGF-beta receptor interacting protein 1 / DB XREF=gi:1036804 / UG=Hs.192023 eukaryotic translation initiation factor 3, subunit 2 (beta, 36kD) / FL=gb:U36764.1 gb:BC000413.1 gb:BC003140.1 gb:U39067.1 gb:NM_003757.1 gb:AF116697.1
200684_s_at	Consensus includes gb:AB023216.1 / DEF=Homo sapiens mRNA for KIAA0999 protein, partial cds. / FEA=mrna / GEN=KIAA0999 / PROD=KIAA0999 protein / DB XREF=gi:4589641 / UG=Hs.4278 KIAA0999 protein
213019_at	Consensus includes gb:A1819709 / FEA=EST / DB XREF=gi:5438788 / DB XREF=est:wj77c07.x1 / CLONE=IMAGE:2408844 / UG=Hs.108104 ubiquitin-conjugating enzyme E2L3 / FL=gb:NM_003347.1
218617_at	Consensus includes gb:A1123233 / FEA=EST / DB XREF=gi:3538999 / DB XREF=est:qa47e04.x1 / CLONE=IMAGE:1689918 / UG=Hs.167496 RAN binding protein 6
	gb:NM_017646.1 / DEF=Homo sapiens tRNA isopentenylpyrophosphate transferase (IPT), mRNA. / FEA=mrna / GEN=IPT / PROD=tRNA isopentenylpyrophosphate transferase / DB XREF=gi:8923064 / UG=Hs.288036 tRNA isopentenylpyrophosphate transferase /

	FL-gb:NM_017646.1	
208308_s_at	gb:NM_000175.1 /DEF=Homo sapiens glucose phosphate isomerase (GPI), mRNA. /FEA=mrna /GEN=GPI /PROD=glucose phosphate isomerase /DB_XREF=gi:4504086 /UG=Hs.180532 glucose phosphate isomerase /FL=gb:BC004982.1 gb:K03515.1 gb:NM_000175.1	
209429_x_at	gb:AF112207.1 /DEF=Homo sapiens translation initiation factor eIF-2b delta subunit mRNA, complete cds. /FEA=mrna /PROD=translation initiation factor eIF-2b delta subunit /DB_XREF=gi:6563201 /UG=Hs.169474 DKFZP586J0119 protein /FL=gb:BC001870.1 gb:AF112207.1	
221501_x_at	gb:AF229069.1 /DEF=Homo sapiens KIAA0220-like protein mRNA, complete cds. /FEA=mrna /PROD=KIAA0220-like protein /DB_XREF=gi:8980670 /UG=Hs.251928 nuclear pore complex interacting protein /FL=gb:AF229069.1	
209161_at	Consensus includes gb:AI184802 /FEA=EST /DB_XREF=gi:3735440 /DB_XREF=est:q24q04.xl /CLONE=IMAGE:1724694 /UG=Hs.8551 PRP4STRWD splicing factor /FL=gb:AF016369.1 gb:U82756.1 gb:NM_004697.1	
201414_s_at	gb:NM_005969.1 /DEF=Homo sapiens nucleosome assembly protein 1-like 4 (NAP1L4), mRNA. /FEA=mrna /GEN=NAP1L4 /PROD=nucleosome assembly protein 1-like 4 /DB_XREF=gi:5174612 /UG=Hs.78103 nucleosome assembly protein 1-like 4 /FL=gb:U77456.1 gb:NM_005969.1	
212361_s_at	Consensus includes gb:AW190070 /FEA=EST /DB_XREF=gi:6464550 /DB_XREF=est:x111f11.xl /CLONE=IMAGE:2675949 /UG=Hs.1526 ATPase, Ca++ transporting, cardiac muscle, slow twitch 2	
204084_s_at	Consensus includes gb:AI911687 /FEA=EST /DB_XREF=gi:5631542 /DB_XREF=est:wc7lq01.xl /CLONE=IMAGE:2324112 /UG=Hs.30213 ceroid-lipofuscinosis, neuronal 5 /FL=gb:AF068227.1 gb:NM_006493.1	
203200_s_at	gb:NM_024010.1 /DEF=Homo sapiens 5-methyltetrahydrofolate-homocysteine methyltransferase reductase (MTRR), transcript variant 2, mRNA. /FEA=mrna /GEN=MTRR /PROD=5-methyltetrahydrofolate-homocysteine methyltransferase reductase, isoform 2 /DB_XREF=gi:13325067 /UG=Hs.153792 5-methyltetrahydrofolate-homocysteine methyltransferase reductase /FL=gb:NM_024010.1 gb:AF121214.1	
201405_s_at	gb:NM_006833.1 /DEF=Homo sapiens COP9 subunit 6 (MOV34 homolog, 34 kd) (MOV34-34KD), mRNA. /FEA=mrna /GEN=MOV34-34KD /PROD=COP9 subunit 6 (MOV34 homolog, 34 kd) /DB_XREF=gi:5803095 /UG=Hs.15591 COP9 subunit 6 (MOV34 homolog, 34 kd) /FL=gb:BC002520.1 gb:U70735.1 gb:NM_006833.1	
218556_at	gb:NM_014182.1 /DEF=Homo sapiens HSPC160 protein (HSPC160), mRNA. /FEA=mrna /GEN=HSPC160 /PROD=HSPC160 protein /DB_XREF=gi:7661819 /UG=Hs.13144 HSPC160 protein /FL=gb:AF161509.1 gb:NM_014182.1	
217756_x_at	gb:NM_005770.1 /DEF=Homo sapiens small EDRK-rich factor 2 (SERF2), mRNA. /FEA=mrna /GEN=SERF2 /PROD=small EDRK-rich factor 2 /DB_XREF=gi:5032084 /UG=Hs.323806 small EDRK-rich factor 2 /FL=gb:AF320073.1 gb:AF073298.1 gb:NM_005770.1	
209206_at	Consensus includes gb:AV701283 /FEA=EST /DB_XREF=gi:10717613 /DB_XREF=est:AV701283 /CLONE=ADAAGD06 /UG=Hs.50785 SEC22, vesicle trafficking protein (S. cerevisiae)-like 1 /FL=gb:BC001364.1 gb:AF047442.1 gb:NM_004892.1	
212165_at	Consensus includes gb:AF070537.1 /DEF=Homo sapiens clone 24606 mRNA sequence. /FEA=mrna /DB_XREF=gi:3387894 /UG=Hs.17481 Homo sapiens clone 24606 mRNA sequence	
208983_s_at	gb:M37780.1 /DEF=Human leukocyte surface protein (CD31), complete cds. /FEA=mrna /GEN=CD31 /PROD=leukocyte surface protein /DB_XREF=gi:187239 /UG=Hs.78146 plateletendothelial cell adhesion molecule (CD31 antigen) /FL=gb:M37780.1 gb:M28526.1 gb:NM_000442.1	
202042_at	gb:NM_002109.2 /DEF=Homo sapiens histidyl-tRNA synthetase (HARS), mRNA. /FEA=mrna /GEN=HARS /PROD=histidyl tRNA synthetase /DB_XREF=gi:6996013 /UG=Hs.77798 histidyl-tRNA synthetase /FL=gb:NM_002109.2	
202433_at	gb:NM_005827.1 /DEF=Homo sapiens UDP-galactose transporter related (UGTREL1), mRNA. /FEA=mrna /GEN=UGTREL1 /PROD=UDP-galactose transporter related /DB_XREF=gi:5032212 /UG=Hs.154073 UDP-galactose transporter related /FL=gb:D87989.1 gb:NM_005827.1	
201145_at	gb:NM_006118.2 /DEF=Homo sapiens HSI binding protein (HAX1), mRNA. /FEA=mrna /GEN=HAX1 /PROD=HSI binding protein /DB_XREF=gi:13435355 /UG=Hs.15318 HSI binding protein /FL=gb:NM_006118.2 gb:BC005240.1 gb:U68566.1	
211975_at	Consensus includes gb:BE299671 /FEA=EST /DB_XREF=gi:9183419 /DB_XREF=est:600944342T1 /CLONE=IMAGE:2960218 /UG=Hs.256310 protein kinase C and casein kinase substrate in neurons 3	
200918_s_at	gb:NM_003139.1 /DEF=Homo sapiens signal recognition particle receptor (docking protein) (SRPR), mRNA. /FEA=mrna /GEN=SRPR /PROD=signal recognition particle receptor (docking protein) /DB_XREF=gi:4507222 /UG=Hs.15730 signal recognition particle receptor (docking protein) /FL=gb:BC001162.1 gb:NM_003139.1	
203497_at	gb:NM_004774.1 /DEF=Homo sapiens PPAR binding protein (PPARBP), mRNA. /FEA=mrna /GEN=PPARBP /PROD=thyroid hormone receptor interactor 2 /DB_XREF=gi:4759265 /UG=Hs.15589 PPAR binding protein /FL=gb:AF055994.1 gb:NM_004774.1 gb:AF283812.1	
209153_s_at	gb:M31523.1 /DEF=Human transcription factor (E2A) mRNA, complete cds. /FEA=mrna /GEN=TCF3 /DB_XREF=gi:339477 /UG=Hs.101047 transcription factor 3 (E2A immunoglobulin enhancer binding factors E12E47) /FL=gb:M31523.1	
220966_x_at	gb:NM_030978.1 /DEF=Homo sapiens hypothetical protein similar to actin related protein 23 complex, subunit 5 (MGC3038), mRNA. /FEA=mrna /GEN=MGC3038 /PROD=hypothetical protein similar to actin related protein 23 complex, subunit 5 /DB_XREF=gi:13569955 /FL=gb:NM_030978.1	

212785_s_at	Consensus includes gb:AA160181 /FEA=EST /DB_XREF=gi:1734757 /DB_XREF=est:zo81d09.s1 /CLONE=IMAGE:593297 /UG=Hs.278635 HDCM18P protein
219176_at	gb:NM_024520.1 /DEF=Homo sapiens hypothetical protein FLJ22555 (FLJ22555), mRNA. /FEA=mrna /GEN=FLJ22555 /PROD=hypothetical protein FLJ22555 /UG=Hs.3592 hypothetical protein FLJ22555 /FE=gb:NM_024520.1
218679_s_at	gb:NM_016208.1 /DEF=Homo sapiens VPS28 protein (LOC51160), mRNA. /FEA=mrna /GEN=LOC51160 /PROD=VPS28 protein /DB_XREF=gi:7705884 /UG=Hs.293441 VPS28 protein (LOC51160), mRNA. /FEA=mrna /GEN=LOC51160 /PROD=VPS28 protein /FE=gb:AF182844.1 gb:NM_016208.1
206991_s_at	gb:NM_000579.1 /DEF=Homo sapiens chemokine (C-C motif) receptor 5 (CCR5), mRNA. /FEA=mrna /GEN=CCR5 /PROD=chemokine (C-C motif) receptor 5 /DB_XREF=gi:4502638 /UG=Hs.54443 chemokine (C-C motif) receptor 5 /FE=gb:U54994.1 gb:U57840.1 gb:NM_000579.1
209770_at	gb:U090552.1 /DEF=Human butyrophilin (BTFF5) mRNA, complete cds. /FEA=mrna /GEN=BTFF5 /PROD=butyrophilin /DB_XREF=gi:2062705 /UG=Hs.284283 butyrophilin, subfamily 3, member A1 /FE=gb:U90552.1
214268_s_at	Consensus includes gb:AL042220 /FEA=EST /DB_XREF=gi:5421564 /DB_XREF=est:DKFZp434H1920_s1 /CLONE=DKFZp434H1920 /UG=Hs.141727 myotubularin related protein 4
201885_s_at	gb:NM_000398.3 /DEF=Homo sapiens diaphorase (NADH) (cytochrome b-5 reductase) (DIAL1), nuclear gene encoding mitochondrial protein, transcript variant M, mRNA. /FEA=mrna /GEN=DIAL1 /PROD=cytochrome b5 reductase, membrane-bound isoform /DB_XREF=gi:6552326 /UG=Hs.274464 diaphorase (NADH) (cytochrome b-5 reductase) /FE=gb:BC004821.1 gb:NM_000398.3
209688_s_at	gb:BC005078.1 /DEF=Homo sapiens, clone MGC:13033, mRNA, complete cds. /FEA=mrna /PROD=Unknown (protein for MGC:13033) /DB_XREF=gi:13471224 /UG=Hs.26118 Homo sapiens clone 24766 mRNA sequence /FE=gb:BC005078.1
203487_s_at	gb:NM_015396.1 /DEF=Homo sapiens DKFZP434A043 protein (DKFZP434A043), mRNA. /FEA=mrna /GEN=DKFZP434A043 /PROD=DKFZP434A043 protein /DB_XREF=gi:7661561 /UG=Hs.102708 DKFZP434A043 protein /FE=gb:NM_015396.1
202155_s_at	gb:NM_005085.1 /DEF=Homo sapiens nucleoporin 214kD (CAIN) (NUP214), mRNA. /FEA=mrna /GEN=NUP214 /PROD=nucleoporin 214kD (CAIN) /DB_XREF=gi:4826873 /UG=Hs.170285 nucleoporin 214kD (CAIN) /FE=gb:NM_005085.1
221786_at	Consensus includes gb:BF197222 /FEA=EST /DB_XREF=gi:11085906 /DB_XREF=est:7m88b07.x1 /CLONE=IMAGE:3561949 /UG=Hs.12342 Homo sapiens clone 24538 mRNA sequence
212846_at	Consensus includes gb:AA811192 /FEA=EST /DB_XREF=gi:2880803 /DB_XREF=est:ob72b08.s1 /CLONE=IMAGE:1336887 /UG=Hs.152629 KIAA0179 protein
209444_at	gb:BC001851.1 /DEF=Homo sapiens, Similar to RAP1, GTP-GDP dissociation stimulator 1, clone MGC:4525, mRNA, complete cds. /FEA=mrna /PROD=Similar to RAP1, GTP-GDP dissociation stimulator 1 /DB_XREF=gi:12804812 /UG=Hs.7940 RAP1, GTP-GDP dissociation stimulator 1 /FE=gb:NM_021159.1 gb:BC001851.1 gb:BC001816.1 gb:AF215923.1 gb:AF237413.1
211937_at	Consensus includes gb:NM_001417.1 /DEF=Homo sapiens eukaryotic translation initiation factor 4B (EIF4B), mRNA. /FEA=cds /GEN=EIF4B /PROD=eukaryotic translation initiation factor 4B /DB_XREF=gi:4503532 /UG=Hs.93379 eukaryotic translation initiation factor 4B /FE=gb:NM_001417.1
201800_s_at	gb:AF185696.1 /DEF=Homo sapiens oxysterol-binding protein 1 (OSBP1) mRNA, complete cds. /FEA=mrna /GEN=OSBP1 /PROD=oxysterol-binding protein 1 /DB_XREF=gi:10441379 /UG=Hs.24734 oxysterol binding protein /FE=gb:AF185696.1 gb:M86917.1
211730_s_at	gb:BC005903.1 /DEF=Homo sapiens, polymerase (RNA) II (DNA directed) polypeptide L (7.6kD), clone MGC:14494, mRNA, complete cds. /FEA=mrna /PROD=polymerase (RNA) II (DNA directed) polypeptide L (7.6kD) /DB_XREF=gi:13543491 /FE=gb:BC005903.1
65635_at	Cluster Incl. AL044097:DKFZp434M1928_s1 Homo sapiens cDNA, 3' end /clone=DKFZp434M1928 /clone_end=3 /gb=AL044097 /gi=5432324 /ug=Hs.29288 /len=605
207438_s_at	gb:NM_005701.1 /DEF=Homo sapiens RNA, U transporter 1 (RNU1), mRNA. /FEA=mrna /GEN=RNU1 /PROD=RNA, U transporter 1 /DB_XREF=gi:5031832 /UG=Hs.21577 RNA, U transporter 1 /FE=gb:AF039029.1 gb:NM_005701.1
221819_at	Consensus includes gb:BF791960 /FEA=EST /DB_XREF=gi:12097014 /DB_XREF=est:602252342FI /CLONE=IMAGE:4344539 /UG=Hs.94308 Homo sapiens cDNA FLJ10447 fts, clone NT2RT100081
203912_s_at	gb:NM_006730.1 /DEF=Homo sapiens deoxyribonuclease I-like 1 (DNASE1L1), mRNA. /FEA=mrna /GEN=DNASE1L1 /PROD=deoxyribonuclease I-like 1 /DB_XREF=gi:5803006 /UG=Hs.77091 deoxyribonuclease I-like 1 /FE=gb:U06846.1 gb:NM_006730.1
216996_s_at	Consensus includes gb:AK021557.1 /DEF=Homo sapiens cDNA FLJ11495 fts, clone HEMBA1001950, highly similar to Homo sapiens mRNA for KIAA0971 protein. /FEA=mrna /DB_XREF=gi:10432760 /UG=Hs.84429 KIAA0971 protein
202138_x_at	gb:NM_006303.2 /DEF=Homo sapiens JTV1 gene (JTV1), mRNA. /FEA=mrna /GEN=JTV1 /PROD=JTV1 /DB_XREF=gi:11125769 /UG=Hs.301613 JTV1 gene /FE=gb:NM_006303.2 gb:U24169.1 gb:BC002853.1
219007_at	gb:NM_024647.1 /DEF=Homo sapiens hypothetical protein FLJ13287 (FLJ13287), mRNA. /FEA=mrna /GEN=FLJ13287 /PROD=hypothetical protein FLJ13287 /DB_XREF=gi:13375888 /UG=Hs.53263 hypothetical protein FLJ13287 /FE=gb:NM_024647.1
219714_s_at	gb:NM_018398.1 /DEF=Homo sapiens calcium channel alpha2-delta3 subunit (HSA272268), mRNA. /FEA=mrna /GEN=HSA272268 /PROD=calcium channel alpha2-delta3 subunit /DB_XREF=gi:8923764 /UG=Hs.22958 calcium channel, voltage-dependent, alpha 2delta 3

201263_at	subunit /FL-gb:NM_018398.1
201157_s_at	gb:NM_003191.1 /DEF-Homo sapiens threonyl-tRNA synthetase (TARS), mRNA. /FEA-mRNA /GEN-TARS /PROD-threonyl-tRNA synthetase /DB_XREF-gi:4507366 /UG-Hs.84131 threonyl-tRNA synthetase /FL-gb:BC000517.1 gb:M63180.1 gb:NM_003191.1 Consensus includes gb:AF020500.1 /DEF-Homo sapiens myristoyl CoA:protein N-myristoyltransferase mRNA, complete cds. /FEA-CDS /PROD-myristoyl CoA:protein N-myristoyltransferase /DB_XREF-gi:2760893 /UG-Hs.111039 N-myristoyltransferase 1 /FL-gb:NM_021079.1 gb:AF020500.1 gb:AF043324.1
221593_s_at	gb:BC001663.1 /DEF-Homo sapiens, Similar to ribosomal protein L31, clone MGC:1641, mRNA, complete cds. /FEA-mRNA /PROD-Similar to ribosomal protein L31 /DB_XREF-gi:12804504 /UG-Hs.164170 vascular Rab-GAPTBC-containing /FL-gb:BC001663.1 Consensus includes gb:N21364 /FEA-EST /DB_XREF-gi:1126534 /DB_XREF-est:ys50h10.s1 /CLONE-IMAGE:265219 /UG-Hs.26968 Homo sapiens mRNA from chromosome 5q21-22, clone:357Ex
214202_at	gb:NM_003664.1 /DEF-Homo sapiens adaptor-related protein complex 3, beta 1 subunit /DB_XREF-gi:4501974 /GEN-AP3B1 /PROD-adaptor-related protein complex 3, beta 1 subunit /FL-gb:U91931.1 gb:U81504.1 gb:NM_003664.1 /UG-Hs.155172 adaptor-related protein complex 3, beta 1 subunit /FEA-EST /DB_XREF-est:qbs1h08.x1 /CLONE-IMAGE:1703679 /UG-Hs.295901
222001_x_at	Consensus includes gb:AI160126 /FEA-EST /DB_XREF-gi:3693506 /DB_XREF-est:qbs1h08.x1 /CLONE-IMAGE:1703679 /UG-Hs.295901 KIAA0493 protein
213374_x_at	Consensus includes gb:AW000964 /FEA-EST /DB_XREF-gi:5847880 /DB_XREF-est:wr90h10.x1 /CLONE-IMAGE:2495011 /UG-Hs.236642 3-hydroxyisobutyryl-Coenzyme A hydrolase
201018_at	Consensus includes gb:AL079283.1 /DEF-Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 39515. /FEA-mRNA /DB_XREF-gi:5102744 /UG-Hs.4310 eukaryotic translation initiation factor 1A /FL-gb:BC000793.1 gb:LI8960.1 gb:NM_001412.1
206206_at	gb:NM_005582.1 /DEF-Homo sapiens lymphocyte antigen 64 (mouse) homolog, radioprotective, 105kd (LY64), mRNA. /FEA-mRNA /GEN-LY64 /PROD-lymphocyte antigen 64 (mouse) homolog, radioprotective, 105kd /DB_XREF-gi:5031894 /UG-Hs.87205 lymphocyte antigen 64 (mouse) homolog, radioprotective, 105kd /FL-gb:DB3597.1 gb:NM_005582.1
209566_at	Consensus includes gb:AL080184.1 /DEF-Homo sapiens mRNA; cDNA DRF2p4340071 (from clone DRF2p4340071). /FEA-mRNA /DB_XREF-gi:5262661 /UG-Hs.7089 insulin induced protein 2 /FL-gb:AF125392.1
212194_s_at	Consensus includes gb:AI418892 /FEA-EST /DB_XREF-gi:4264823 /DB_XREF-est:tf43c01.x1 /CLONE-IMAGE:2098944 /UG-Hs.79305 KIAA0255 gene product
204526_s_at	gb:NM_007063.1 /DEF-Homo sapiens vascular Rab-GAPTBC-containing (VRP), mRNA. /FEA-mRNA /GEN-VRP /PROD-vascular Rab-GAPTBC-containing /DB_XREF-gi:5902153 /UG-Hs.164170 vascular Rab-GAPTBC-containing /FL-gb:AB024057.1 gb:NM_007063.1
201568_at	gb:NM_014402.1 /DEF-Homo sapiens low molecular mass ubiquinone-binding protein (9.5kd) (QP-C), mRNA. /FEA-mRNA /GEN-QP-C /PROD-low molecular mass ubiquinone-binding protein /DB_XREF-gi:7657485 /UG-Hs.3709 low molecular mass ubiquinone-binding protein (9.5kd) /FL-gb:BC001390.1 gb:D50369.1 gb:NM_014402.1
221829_s_at	Consensus includes gb:AI307759 /FEA-EST /DB_XREF-gi:4002363 /DB_XREF-est:tb24g08.x1 /CLONE-IMAGE:2055326 /UG-Hs.168075 karyopherin (importin) beta 2
200613_at	gb:NM_004068.1 /DEF-Homo sapiens adaptor-related protein complex 2, mu 1 subunit (AP2M1), mRNA. /FEA-mRNA /GEN-AP2M1 /PROD-adaptor-related protein complex 2, mu 1 subunit /DB_XREF-gi:4757993 /UG-Hs.152936 adaptor-related protein complex 2, mu 1 subunit /FL-gb:U36188.1 gb:BC004996.1 gb:D63475.1 gb:NM_004068.1
213160_at	Consensus includes gb:DB6964.1 /DEF-Human mRNA for KIAA0209 gene, partial cds. /FEA-mRNA /GEN-KIAA0209 /DB_XREF-gi:1504001 /UG-Hs.17211 dedicator of cyto-kinesis 2
211375_s_at	gb:AF141870.1 /DEF-Homo sapiens translational control protein 80 mRNA, complete cds. /FEA-mRNA /PROD-translational control protein 80 /DB_XREF-gi:5006601 /UG-Hs.256583 interleukin enhancer binding factor 3, 90kd /FL-gb:AF141870.1
202276_at	gb:NM_006304.1 /DEF-Homo sapiens Deleted in split-handsplit-foot 1 region (DSS1), mRNA. /FEA-mRNA /GEN-DSS1 /PROD-deleted in split-handsplit-foot 1 region /DB_XREF-gi:5453639 /UG-Hs.85215 Deleted in split-handsplit-foot 1 region /FL-gb:U41515.1 gb:NM_006304.1
201892_s_at	gb:NM_000884.1 /DEF-Homo sapiens IMP (inosine monophosphate) dehydrogenase 2 (IMPDH2), mRNA. /FEA-mRNA /GEN-IMPDH2 /PROD-IMP (inosine monophosphate) dehydrogenase 2 /DB_XREF-gi:4504688 /UG-Hs.75432 IMP (inosine monophosphate) dehydrogenase 2 /FL-gb:U04208.1 gb:NM_000884.1
217905_at	gb:NM_024834.1 /DEF-Homo sapiens hypothetical protein FLJ13081 (FLJ13081), mRNA. /FEA-mRNA /GEN-FLJ13081 /PROD-hypothetical protein FLJ13081 /DB_XREF-gi:13376242 /UG-Hs.180638 hypothetical protein FLJ13081 /FL-gb:BC004183.1 gb:NM_024834.1
209036_s_at	gb:BC001917.1 /DEF-Homo sapiens, malate dehydrogenase 2, NAD (mitochondrial), clone MGC:3559, mRNA, complete cds. /FEA-mRNA /PROD-malate dehydrogenase 2, NAD (mitochondrial) /DB_XREF-gi:12804928 /UG-Hs.111076 malate dehydrogenase 2, NAD (mitochondrial) /FL-gb:BC001917.1 gb:AF047470.1 gb:NM_005918.1

222010_at	Consensus includes gb:BF224073 /FEA=EST /DB_XREF=gi:11131299 /DB_XREF=est:7q83e05.x1 /CLONE=IMAGE:3704936 /UG=Hs.278544 acetyl-Coenzyme A acetyltransferase 2 (acetoacetyl Coenzyme A thiolase)
203825_at	gb:NM_007371.2 /DEF=Homo sapiens bromodomain-containing 3 (BRD3), mRNA. /FEA=mrna /GEN=BRD3 /PROD=bromodomain-containing protein 3 /DB_XREF=gi:12408642 /UG=Hs.86896 bromodomain-containing 3 /FL=gb:NM_007371.2 gb:D26362.1
202943_s_at	gb:M38083.1 /DEF=human alpha-N-acetylgalactosaminidase mRNA, complete cds. /FEA=mrna /PROD=alpha-N-acetylgalactosaminidase /DB_XREF=gi:189054 /UG=Hs.75372 N-acetylgalactosaminidase, alpha- /FL=gb:BC000095.1 gb:M38083.1 gb:NM_000262.1
210555_s_at	gb:U85430.1 /DEF=Human transcription factor NFATx4 mRNA, complete cds. /FEA=mrna /PROD=transcription factor NFATx4 /DB_XREF=gi:1835590 /UG=Hs.172674 nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 3 /FL=gb:U85430.1
218370_s_at	gb:NM_022753.1 /DEF=Homo sapiens hypothetical protein FLJ12903 (FLJ12903), mRNA. /FEA=mrna /GEN=FLJ12903 /PROD=hypothetical protein FLJ12903 /FL=gb:NM_022753.1
208070_s_at	gb:NM_002912.1 /DEF=Homo sapiens REV3 (yeast homolog)-like, catalytic subunit of DNA polymerase zeta (REV3L), mRNA. /FEA=mrna /GEN=REV3L /PROD=REV3 (yeast homolog)-like, catalytic subunit of DNA polymerase zeta /DB_XREF=gi:4506482 /UG=Hs.115521 REV3 (yeast homolog)-like, catalytic subunit of DNA polymerase zeta /FL=gb:AF078695.1 gb:NM_002912.1 gb:AF179428.1
201272_at	gb:NM_001628.1 /DEF=Homo sapiens aldo-keto reductase family 1, member B1 (aldose reductase) (AKR1B1), mRNA. /FEA=mrna /GEN=AKR1B1 /PROD=aldo-keto reductase family 1, member B1 (aldose reductase) /DB_XREF=gi:4502048 /UG=Hs.75313 aldo-keto reductase family 1, member B1 (aldose reductase) /FL=gb:BC000260.1 gb:BC0005387.1 gb:J04795.1 gb:J05017.1 gb:J05474.1 gb:M34720.1
209824_s_at	gb:AB000812.1 /DEF=Homo sapiens mRNA for BML1b, complete cds. /FEA=mrna /PROD=BML1b /DB_XREF=gi:2094734 /UG=Hs.74515 aryl hydrocarbon receptor nuclear translocator-like /FL=gb:AB000812.1 gb:AF044288.1
209064_x_at	gb:AL136920.1 /DEF=Homo sapiens mRNA; cDNA DKFp586C051 (from clone DKFp586C051); complete cds. /FEA=mrna /GEN=DKFp586C051 /PROD=hypothetical protein /DB_XREF=gi:12053334 /UG=Hs.109643 polyadenylate binding protein-interacting protein 1 /FL=gb:AL136920.1
200759_x_at	gb:NM_003204.1 /DEF=Homo sapiens nuclear factor (erythroid-derived 2)-like 1 (NFE2L1), mRNA. /FEA=mrna /GEN=NFE2L1 /PROD=transcription factor 11 (basic leucine zipper type) /DB_XREF=gi:4505378 /UG=Hs.83469 nuclear factor (erythroid-derived 2)-like 1 /FL=gb:NM_003204.1 gb:U08853.1
221787_at	Consensus includes gb:BF431618 /FEA=EST /DB_XREF=gi:11443732 /DB_XREF=est:7o16e03.x1 /CLONE=IMAGE:3574349 /UG=Hs.12342 Homo sapiens clone 24538 mRNA sequence
211581_x_at	gb:AF000426.1 /DEF=Homo sapiens LST1 mRNA, cDNA splice variant, complete cds. /FEA=mrna /GEN=LST1 /DB_XREF=gi:2145067 /UG=Hs.88411 lymphocyte antigen 117 /FL=gb:AF000426.1
37384_at	Cluster Incl. D13640:Human mRNA for KIAA0015 gene, complete cds /cds=(106,1470) /gb=D13640 /gi=286006 /ug=Hs.77961 /len=5134
218423_x_at	gb:NM_016516.1 /DEF=Homo sapiens tumor antigen SLP-8p (HCC8), mRNA. /FEA=mrna /GEN=HCC8 /PROD=tumor antigen SLP-8p /DB_XREF=gi:7705396 /UG=Hs.48499 tumor antigen SLP-8p /FL=gb:AF102177.1 gb:NM_016516.1
210213_s_at	gb:AF022229.1 /DEF=Homo sapiens translation initiation factor 6 (eIF6) mRNA, complete cds. /FEA=mrna /GEN=eIF6 /PROD=translation initiation factor 6 /DB_XREF=gi:2809382 /UG=Hs.5215 integrin beta 4 binding protein /FL=gb:AF022229.1
201598_s_at	gb:NM_001567.2 /DEF=Homo sapiens inositol polyphosphate phosphatase-like 1 (INPPL1), mRNA. /FEA=mrna /GEN=INPPL1 /PROD=inositol polyphosphate phosphatase-like 1 /DB_XREF=gi:4755141 /UG=Hs.75339 inositol polyphosphate phosphatase-like 1 /FL=gb:NM_001567.2 gb:L2444.1
204301_at	gb:NM_014867.1 /DEF=Homo sapiens KIAA0711 gene product (KIAA0711), mRNA. /FEA=mrna /GEN=KIAA0711 /PROD=KIAA0711 gene product /DB_XREF=gi:7662259 /UG=Hs.5333 KIAA0711 gene product /FL=gb:AB018254.1 gb:NM_014867.1
202877_s_at	Consensus includes gb:W72082 /FEA=EST /DB_XREF=gi:1382588 /DB_XREF=est:zd70c06.s1 /CLONE=IMAGE:345994 /UG=Hs.97199 complement component C1q receptor /FL=gb:NM_012072.2 gb:U94333.1
208772_at	Consensus includes gb:AU160676 /FEA=EST /DB_XREF=gi:11022197 /DB_XREF=est:AU160676 /CLONE=Y79AA1002208 /UG=Hs.301226 KIAA1085 protein /FL=gb:AL136943.1
201998_at	Consensus includes gb:AI743792 /FEA=EST /DB_XREF=gi:5112080 /DB_XREF=est:wq53h11.x1 /CLONE=IMAGE:2368869 /UG=Hs.2554 sialyltransferase 1 (beta-galactoside alpha-2,6-sialyltransferase) /FL=gb:NM_003032.1
208722_s_at	gb:BC001081.1 /DEF=Homo sapiens, anaphase-promoting complex subunit 5, clone MGC:2750, mRNA, complete cds. /FEA=mrna /PROD=anaphase-promoting complex subunit 5 /DB_XREF=gi:12654502 /UG=Hs.7101 anaphase-promoting complex subunit 5 /FL=gb:BC001081.1 gb:BC001950.1 gb:AF191339.1 gb:NM_016237.1
55692_at	Cluster Incl. W22924:75H3 Homo sapiens cDNA /clone=(not-directional) /gb=W22924 /gi=1299757 /ug=Hs.96560 /len=792
217954_s_at	gb:NM_015153.1 /DEF=Homo sapiens KIAA0244 protein (KIAA0244), mRNA. /FEA=mrna /GEN=KIAA0244 /PROD=KIAA0244 protein /DB_XREF=gi:7662017 /UG=Hs.78893 KIAA0244 protein /FL=gb:AF091622.1 gb:NM_015153.1

220307_at	gb:NM_016382.1 /DEF=Homo sapiens natural killer cell receptor 2B4 (CD244), mRNA. /FEA=mrna /GEN=CD244 /PROD=natural killer cell receptor 2B4 /DB_XREF=gi:7706528 /UG=Hs.157872 natural killer cell receptor 2B4 /FL=gb:AF105261.1 gb:AF145782.1 gb:AF107761.2 gb:AF117711.1 gb:NM_016382.1
211989_at	Consensus includes gb:NM_003079.1 /DEF=Homo sapiens SWISNF related, matrix associated, actin dependent regulator of chromatin, subfamily e, member 1 (SMARCE1), mRNA. /FEA=cds /GEN=SMARCE1 /PROD=SWISNF related, matrix associated, actin dependent regulator of chromatin, subfamily e, member 1 /DB_XREF=gi:4507088 /UG=Hs.332848 SWISNF related, matrix associated, actin dependent regulator of chromatin, subfamily e, member 1 /FL=gb:NM_003079.1
209303_at	gb:BC005270.1 /DEF=Homo sapiens, NADH dehydrogenase (ubiquinone) Fe-S protein 4 (18kD) (NADH-coenzyme Q reductase), clone MGC:12313, mRNA, complete cds. /FEA=mrna /PROD=NADH dehydrogenase (ubiquinone) Fe-S protein 4 (18kD) (NADH-coenzyme Q reductase) /DB_XREF=gi:13528959 /UG=Hs.10758 NADH dehydrogenase (ubiquinone) Fe-S protein 4 (18kD) (NADH-coenzyme Q reductase) /FL=gb:BC005270.1 gb:AF020351.1 gb:NM_002495.1
201729_s_at	gb:NM_014680.1 /DEF=Homo sapiens KIAA0100 gene product (KIAA0100), mRNA. /FEA=mrna /GEN=KIAA0100 /PROD=KIAA0100 gene product /DB_XREF=gi:7661903 /UG=Hs.151761 KIAA0100 gene product /FL=gb:D43947.1 gb:NM_014680.1
203530_s_at	gb:NM_004604.1 /DEF=Homo sapiens syntaxin 4A (placental) (STX4A), mRNA. /FEA=mrna /GEN=STX4A /PROD=syntaxin 4A (placental) /DB_XREF=gi:4759185 /UG=Hs.83734 syntaxin 4A (placental) /FL=gb:BC002436.1 gb:AF026007.1 gb:U07158.1 gb:NM_004604.1
201622_at	gb:NM_014390.1 /DEF=Homo sapiens EBNA-2 co-activator (100kD) (p100), mRNA. /FEA=mrna /GEN=p100 /PROD=EBNA-2 co-activator (100kD) /DB_XREF=gi:7657430 /UG=Hs.79093 EBNA-2 co-activator (100kD) /FL=gb:NM_014390.1 gb:U22055.1

Tabelle 2: Gene aus Clusteranalyse 2

Affymetrix-interne Bezeichnung	Beschreibung der Sequenz in der GeneBank Datenbank
200654_at	gb:J02783.1 /DEF=human thyroid hormone binding protein (p55) mRNA, complete cds. /FEA=mRNA /GEN=P4HB /DB_XREF=gi:339646 /UG=Hs.75655procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), beta polypeptide (protein disulfide isomerase; thyroid hormone binding protein p55) /FL=gb:J02783.1 gb:NM 000918.1
203126_at	gb:NM 014214.1 /DEF=Homo sapiens inositol (myo)-1(or 4)-monophosphatase 2 (IMPA2), mRNA. /FEA=mRNA /GEN=IMPA2 /PROD=inositol (myo)-1(or 4)-monophosphatase 2 /DB_XREF=gi:1657235 /UG=Hs.5753 inositol (myo)-1(or 4)-monophosphatase 2 /FL=gb:AF200432.1 gb:NM 014214.1 gb:AF014398.2
203585_at	gb:NM 007150.1 /DEF=Homo sapiens zinc finger protein 185 (LIM domain) (ZNF185), mRNA. /FEA=mRNA /GEN=ZNF185 /PROD=zinc finger protein 185(LIM domain) /DB_XREF=gi:6005971 /UG=Hs.16622 zinc finger protein 185 (LIM domain) /FL=gb:NM 007150.1
205220_at	gb:NM 006018.1 /DEF=Homo sapiens putative chemokine receptor; GTP-binding protein (HM74), mRNA. /FEA=mRNA /GEN=HM74 /PROD=putative chemokine receptor; GTP-binding protein /DB_XREF=gi:5174460 /UG=Hs.137555 putative chemokine receptor; GTP-binding protein /FL=gb:NM 006018.1
207008_at	gb:NM 001557.1 /DEF=Homo sapiens interleukin 8 receptor, beta (IL8RB), mRNA. /FEA=mRNA /GEN=IL8RB /PROD=interleukin 8 receptor, beta /DB_XREF=gi:4504682 /UG=Hs.846 interleukin 8 receptor, beta (IL8RB), mRNA. /FEA=mRNA /GEN=IL8RB /PROD=interleukin 8 receptor, beta /FL=gb:AF077041.1 gb:AF151909.1 gb:NM 016081.1
200897_s_at	gb:NM 016081.1 /DEF=Homo sapiens plectin (KIAA0992), mRNA. /FEA=mRNA /GEN=KIAA0992 /PROD=palladin /DB_XREF=gi:7706354 / UG=Hs.194431 palladin /FL=gb:AF077041.1 gb:AF151909.1 gb:NM 016081.1
205568_at	gb:NM 020980.2 /DEF=Homo sapiens aquaporin 9 (AQP9), mRNA. /FEA=mRNA /GEN=AQP9 /PROD=aquaporin 9 /DB_XREF=gi:11038652 / UG=Hs.104624 aquaporin 9 /FL=gb:NM 020980.2 gb:AB008775.1 gb:AF016495.1
214022_s_at	Consensus includes gb:AA749101 /FEA=EST /DB_XREF=gi:2789059 /DB_XREF=est:nyl1402.s1 /CLONE=IMAGE:1271427 / UG=Hs.146360 interferon induced transmembrane protein 1 (9-27)
209762_x_at	gb:AF280094.1 /DEF=Homo sapiens transcriptional coactivator Sp110b mRNA, complete cds. /FEA=mRNA /PROD=transcriptional coactivator Sp110b /DB_XREF=gi:9800493 /UG=Hs.38125 interferon-induced protein 75, 52kd /FL=gb:AF280094.1
203234_at	gb:NM 003364.1 /DEF=Homo sapiens uridine phosphorylase (UP), mRNA. /FEA=mRNA /GEN=UP /PROD=uridine phosphorylase /DB_XREF=gi:4507838 /UG=Hs.77573 uridine phosphorylase /FL=gb:BC001405.1 gb:NM 003364.1
201940_at	Consensus includes gb:AA837514 /FEA=EST /DB_XREF=gi:3034134 /DB_XREF=est:aj62612.s1 /CLONE=IMAGE:1394879 /UG=Hs.5057 carboxypeptidase D /FL=gb:U65090.1 gb:NM 001304.2
209310_s_at	gb:U25804.1 /DEF=Human Ich-2 cysteine protease mRNA, complete cds. /FEA=mRNA /PROD=Ich-2 /DB_XREF=gi:886049 /UG=Hs.74122 caspase 4, apoptosis-related cysteine protease /FL=gb:U28976.1 gb:U28977.1 gb:U28978.1 gb:NM 001225.1 gb:U25804.1 gb:U28014.1
202128_at	gb:NM 014821.1 /DEF=Homo sapiens KIAA0317 gene product (KIAA0317), mRNA. /FEA=mRNA /GEN=KIAA0317 /PROD=KIAA0317 gene product /DB_XREF=gi:7682051 /UG=Hs.20126 KIAA0317 gene product /FL=gb:AB002315.1 gb:NM 014821.1
201192_s_at	gb:NM 006224.1 /DEF=Homo sapiens phosphatidylinositol transfer protein (PITPN), mRNA. /FEA=mRNA /GEN=PITPN / PROD=phosphatidylinositol transfer protein /DB_XREF=gi:5453907 /UG=Hs.79709 phosphatidylinositol transfer protein / FL=gb:D30036.1 gb:NM 006224.1
208012_x_at	gb:NM 004509.1 /DEF=Homo sapiens interferon-induced protein 41, 30kd (IFI41), mRNA. /FEA=mRNA /GEN=IFI41 / PROD=interferon-induced protein 41, 30kd /DB_XREF=gi:4758585 /UG=Hs.241510 interferon-induced protein 41, 30kd / FL=gb:L22342.1 gb:NM 004509.1
209137_s_at	gb:BC000263.1 /DEF=Homo sapiens, Similar to ubiquitin c-terminal hydrolase related polypeptide, clone MCC-2621, mRNA, complete cds. /FEA=mRNA /PROD=Similar to ubiquitin c-terminal hydrolase related polypeptide /DB_XREF=gi:12653004 / UG=Hs.78829 ubiquitin specific protease 10 /FL=gb:BC000263.1
218023_s_at	gb:NM 016605.1 /DEF=Homo sapiens putative nuclear protein (LOC51307), mRNA. /FEA=mRNA /GEN=LOC51307 / PROD=putative nuclear protein /DB_XREF=gi:7706138 /UG=Hs.102469 putative nuclear protein /FL=gb:AF251040.1 gb:NM 016605.1
201190_s_at	Consensus includes gb:H15647 /FEA=EST /DB_XREF=gi:880467 /DB_XREF=est:ym27b09.s1 /CLONE=IMAGE:49287 / UG=Hs.79709 phosphatidylinositol transfer protein /FL=gb:D30036.1 gb:NM 006224.1
210563_x_at	gb:U97075.1 /DEF=Homo sapiens FlicE-like inhibitory protein short form mRNA, complete cds. /FEA=mRNA / PROD=FlicE-like inhibitory protein short form /DB_XREF=gi:2253680 /UG=Hs.195175 CASP8 and FADD-like apoptosis regulator /

	FL-gb:U97075.1
221827_at	Consensus includes gb:BE788439 / FEA=EST / DB_XREF=gi:10209637 / DB_XREF=est:601475616f1 / CLONE=IMAGE:3878643 / UG=Hs.247280 HEV associated factor
202041_s_at	gb:NM 004214.3 / DEF=Homo sapiens fibroblast growth factor (acidic) intracellular binding protein (FIBP), mRNA. / FEA=mRNA / GEN=FTBP / PROD=fibroblast growth factor (acidic) intracellular binding protein / DB_XREF=gi:7262377 / UG=Hs.7768 fibroblast growth factor (acidic) intracellular binding protein / FL-gb:AF171944.1 gb:AF171945.1 gb:AF171946.1 gb:AF010187.2 gb:NM 004214.3
201001_s_at	Consensus includes gb:BG164064 / FEA=EST / DB_XREF=gi:12670767 / DB_XREF=est:602341091f1 / CLONE=IMAGE:4443022 / UG=Hs.75875 ublquin-conjugating enzyme E2 variant 1 / FL-gb:U39361.1 gb:NM 003349.2 gb:BC000468.1
212975_at	Consensus includes gb:AB020677.2 / DEF=Homo sapiens mRNA for KIAA0870 protein, partial cds. / FEA=mRNA / GEN=KIAA0870 / PROD=KIAA0870 protein / DB_XREF=gi:6635136 / UG=Hs.18166 KIAA0870 protein
201412_at	gb:NM 014045.1 / DEF=Homo sapiens DKFZP564C1940 protein (DKFZP564C1940), mRNA. / FEA=mRNA / GEN=DKFZP564C1940 / PROD=DKFZP564C1940 protein / DB_XREF=gi:13027587 / UG=Hs.3804 DKFZP564C1940 protein / FL-gb:BC000424.1 gb:NM 014045.1 gb:AF131760.1
203708_at	gb:NM 002600.1 / DEF=Homo sapiens phosphodiesterase 4B, cAMP-specific (dunce (Drosophila)-homolog phosphodiesterase E4 (PDE4B) mRNA. / FEA=mRNA / GEN=PDE4B / PROD=phosphodiesterase 4B, cAMP-specific (dunce (Drosophila)-homolog phosphodiesterase E4 / DB_XREF=gi:4505662 / UG=Hs.188 phosphodiesterase 4B, cAMP-specific (dunce (Drosophila)-homolog phosphodiesterase E4) / FL-gb:M97515.1 gb:L20971.1 gb:NM 002600.1
203907_s_at	gb:NM 014869.1 / DEF=Homo sapiens KIAA0763 gene product (KIAA0763), mRNA. / FEA=mRNA / GEN=KIAA0763 / PROD=KIAA0763 gene product / DB_XREF=gi:7662289 / UG=Hs.4764 KIAA0763 gene product / FL-gb:AB018306.1 gb:NM 014869.1
209882_at	gb:AF084462.1 / DEF=Homo sapiens GTP-binding protein ROC1 (ROC1) mRNA, complete cds. / FEA=mRNA / GEN=ROC1 / PROD=GTP-binding protein ROC1 / DB_XREF=gi:4234917 / UG=Hs.96038 Roc (Drosophila)-like, expressed in many tissues / FL-gb:U71203.1 gb:U78165.1 gb:AF084462.1 gb:NM 006912.1
204276_at	Consensus includes gb:BE895437 / FEA=EST / DB_XREF=gi:10358829 / DB_XREF=est:601437912f1 / CLONE=IMAGE:3922971 / UG=Hs.274701 thymidine kinase 2, mitochondrial / FL-gb:NM 004614.1 gb:U77088.1
221984_s_at	Consensus includes gb:AL040896 / FEA=EST / DB_XREF=gi:5409841 / DB_XREF=est:DKFZP434I2415_s1 / CLONE=DKFZP434I2415 / UG=Hs.22412 hypothetical protein MGC3035
218517_at	gb:NM 024900.1 / DEF=Homo sapiens hypothetical protein FLJ22479 (FLJ22479), mRNA. / FEA=mRNA / GEN=FLJ22479 / PROD=hypothetical protein FLJ22479 / DB_XREF=gi:13376356 / UG=Hs.238246 hypothetical protein FLJ22479 / FL-gb:NM 024900.1
208740_at	Consensus includes gb:BF593650 / FEA=EST / DB_XREF=gi:11685974 / DB_XREF=est:na02403.x1 / CLONE=IMAGE:3275957 / UG=Hs.23964 sin3-associated polypeptide, 18kD / FL-gb:NM 005870.2 gb:U96915.1 gb:AF153608.1 gb:U78303.1
221484_at	Consensus includes gb:BF691447 / FEA=EST / DB_XREF=gi:11976855 / DB_XREF=est:602247615f1 / CLONE=IMAGE:4332866 / UG=Hs.107526 UDP-Gal:betaGALNAc beta 1,4- galactosyltransferase, polypeptide 5 / FL-gb:AB004550.1 gb:AF038663.1 gb:NM 004776.1
209575_at	gb:BC001903.1 / DEF=Homo sapiens, Similar to interleukin 10 receptor, beta, Clone MGC:2210, mRNA, complete cds. / FEA=mRNA / PROD=Similar to interleukin 10 receptor, beta / DB_XREF=gi:12804902 / UG=Hs.173936 interleukin 10 receptor, beta / FL-gb:BC001903.1 gb:NM 000628.1
200619_at	gb:NM 006842.1 / DEF=Homo sapiens splicing factor 3b, subunit 2, 145kD (SF3B2), mRNA. / FEA=mRNA / GEN=SF3B2 / PROD=splicing factor 3b, subunit 2, 145kD / DB_XREF=gi:5803154 / UG=Hs.75916 splicing factor 3b, subunit 2, 145kD / FL-gb:U41371.1 gb:NM 006842.1
217286_s_at	Consensus includes gb:BC001805.1 / DEF=Homo sapiens, clone IMAGE:3543670 / UG=Hs.240615 hypothetical protein FLJ13556 similar to N-myc downstream regulated 3
207842_s_at	gb:NM 007359.1 / DEF=Homo sapiens MLN51 protein (MLN51), mRNA. / FEA=mRNA / GEN=MLN51 / PROD=MLN51 protein / DB_XREF=gi:6678887 / UG=Hs.83422 MLN51 protein / FL-gb:NM 007359.1
217788_s_at	gb:NM 004481.2 / DEF=Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetyl-galactosaminyltransferase 2 (GALNAc-T2) (GALNT2), mRNA. / FEA=mRNA / GEN=GALNT2 / PROD=polypeptide N-acetyl-galactosaminyltransferase 2 / DB_XREF=gi:9945385 / UG=Hs.130181 UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetyl-galactosaminyltransferase 2 (GALNAc-T2) / FL-gb:NM 004481.2
48612_at	Cluster Incl. AA223490:nc25b01.r1 Homo sapiens cDNA / clone=IMAGE-1009129 / gb=AA225490 / gi=1846817 / ug=Hs.80115 / len=539
212689_s_at	Consensus includes gb:AA524505 / FEA=EST / DB_XREF=gi:2265433 / DB_XREF=est:ng43g12.s1 / CLONE=IMAGE:937606 / UG=Hs.321707 KIAA0742 protein

222047_s_at	Consensus includes gb:AI523895 /FEA-EST /DB XREF-gi:4438030 /DB XREF=est:tg97g03.x1 /CLONE=IMAGE:2116756 /UG-Hs.111801 arsenate resistance protein ARS2
201666_at	gb:NM_003254.1 /DEF=Homo sapiens tissue inhibitor of metalloproteinase 1 (erythroid potentiating activity, collagenase inhibitor) (TIMP1), mRNA. /FEA-mRNA /GEN=TIMP1 /PROD=tissue inhibitor of metalloproteinase precursor /DB XREF-gi:4507508 /UG-Hs.5831 tissue inhibitor of metalloproteinase 1 (erythroid potentiating activity, collagenase inhibitor) /FL=gb:BC000866.1 gb:M12670.1 gb:MS9906.1 gb:NM_003254.1
203218_at	Consensus includes gb:W37431 /FEA-EST /DB XREF-gi:1319025 /DB XREF=est:zc11f11.s1 /CLONE=IMAGE:322029 /UG-Hs.246857 mitogen-activated protein kinase 9 /FL=gb:U34821.1 gb:NM_002752.1 gb:L31951.1 gb:U09759.1
213118_at	Consensus includes gb:AL136821.1 /DEF=Homo sapiens mRNA; cDNA DRFZp43M1526 (from clone DRFZp43M1526). /FEA-mRNA /GEN=DRFZp43M1526 /PROD=hypothetical protein /DB XREF-gi:12053152 /UG-Hs.153293 KIAA0701 protein
201057_s_at	gb:NM_004487.1 /DEF=Homo sapiens golgi autoantigen, golgin subfamily b, macrogolin (with transmembrane signal), 1 (GOLGB1), mRNA. /FEA-mRNA /GEN=GOLGB1 /PROD=golgi autoantigen, golgin subfamily b, macrogolin (with transmembrane signal), 1 /DB XREF-gi:4758453 /UG-Hs.7844 golgi autoantigen, golgin subfamily b, macrogolin (with transmembrane signal), 1 /FL=gb:NM_004487.1
217738_at	Consensus includes gb:BE575514 /FEA-EST /DB XREF-gi:11649318 /DB XREF=est:602133090F1 /CLONE=IMAGE:4288079 /UG-Hs.239138 pre-B-cell colony-enhancing factor /FL=gb:U02020.1 gb:NM_005746.1
208648_at	Consensus includes gb:W60953 /FEA-EST /DB XREF-gi:1367731 /DB XREF=est:zc98b12.s1 /CLONE=IMAGE:339167 /UG-Hs.106357 valosin-containing protein /FL=gb:AF100752.1 gb:NM_007126.2
212242_at	Consensus includes gb:AL565074 /FEA-EST /DB XREF-gi:12916087 /DB XREF=est:AL565074 /CLONE=CSODN003YF20 (3 prime) /UG-Hs.75318 tubulin, alpha 1 (testis specific)
203897_at	Consensus includes gb:BE963444 /FEA-EST /DB XREF-gi:11766863 /DB XREF=est:601657224R1 /CLONE=IMAGE:3866357 /UG-Hs.28607 hypothetical protein A-211C6.1 /FL=gb:NM_020424.1
209513_s_at	gb:BC004331.1 /DEF=Homo sapiens, similar to RIKEN cDNA 2610207I16 gene, clone MGC:10940, mRNA, complete cds. /FEA-mRNA /PROD=Similar to RIKEN cDNA 2610207I16 gene /DB XREF-gi:13279253 /UG-Hs.47986 Homo sapiens, similar to RIKEN cDNA 2610207I16 gene, clone MGC:10940, mRNA, complete cds /FL=gb:BC004331.1
211762_s_at	gb:BC005978.1 /DEF=Homo sapiens, karyopherin alpha 2 (RAG cohort 1, importin alpha 1), clone MGC:14668, mRNA, complete cds. /FEA-mRNA /PROD=karyopherin alpha 2 (RAG cohort 1, importin alpha 1) /DB XREF-gi:13543656 /FL=gb:BC005978.1
219639_x_at	gb:NM_020213.1 /DEF=Homo sapiens hypothetical protein from EUROMIMAGE 1977056 [LOC56365], mRNA. /FEA-mRNA /GEN=LOC56365 /PROD=hypothetical protein from EUROMIMAGE 1977056 /DB XREF-gi:1977056 /UG-Hs.315687 hypothetical protein from EUROMIMAGE 1977056 /FL=gb:NM_020213.1
217882_at	gb:NM_018447.1 /DEF=Homo sapiens 30 kDa protein [LOC55831], mRNA. /FEA-mRNA /GEN=LOC55831 /PROD=30 kDa protein /DB XREF-gi:8923856 /UG-Hs.283714 30 kDa protein /FL=gb:AF157321.1 gb:NM_018447.1
204714_s_at	gb:NM_000130.2 /DEF=Homo sapiens coagulation factor V (proaccelerin, labile factor) (F5), mRNA. /FEA-mRNA /GEN=F5 /PROD=coagulation factor V precursor /DB XREF-gi:10518500 /UG-Hs.30054 coagulation factor V (proaccelerin, labile factor) /FL=gb:NM_000130.2 gb:M16967.1 gb:M14335.1
221547_at	gb:BC000794.1 /DEF=Homo sapiens, pre-mRNA splicing factor similar to S. cerevisiae Prp18, clone MGC:5075, mRNA, complete cds. /FEA-mRNA /PROD=pre-mRNA splicing factor similar to S. cerevisiae Prp18 /DB XREF-gi:12653992 /UG-Hs.155244 pre-mRNA processing factor 18 /FL=gb:BC000794.1 gb:U51990.1 gb:NM_003675.1
210793_s_at	gb:U41815.1 /DEF=Human nucleoporin 98 (NUP98) mRNA, complete cds. /FEA-mRNA /GEN=NUP98 /PROD=nucleoporin 98 /DB XREF-gi:1184172 /UG-Hs.112255 nucleoporin 98kD /FL=gb:U41815.1
206207_at	gb:NM_001828.3 /DEF=Homo sapiens Charot-Leyden crystal protein (CLIC), mRNA. /FEA-mRNA /GEN=CLIC /PROD=Charot-Leyden crystal protein /DB XREF-gi:6325464 /UG-Hs.889 Charot-Leyden crystal protein /FL=gb:L01664.1 gb:NM_001828.3
202595_s_at	gb:AF161461.1 /DEF=Homo sapiens HSPC112 mRNA, complete cds. /FEA-mRNA /PROD=HSPC112 /DB XREF-gi:6841445 /UG-Hs.11000 lepton receptor overlapping transcript-like 1 /FL=gb:BC000642.1 gb:AF063605.1 gb:AF161461.1 gb:NM_015344.1
219434_at	gb:NM_018643.1 /DEF=Homo sapiens triggering receptor expressed on myeloid cells 1 (TREM1), mRNA. /FEA-mRNA /GEN=TREM1 /PROD=triggering receptor expressed on myeloid cells /DB XREF-gi:8924261 /UG-Hs.283022 triggering receptor expressed on myeloid cells 1 /FL=gb:AF196329.1 gb:NM_018643.1 gb:AF287008.1
205020_s_at	gb:NM_005738.1 /DEF=Homo sapiens ADP-ribosylation factor-like 4 (ARL4), mRNA. /FEA-mRNA /GEN=ARL4 /PROD=ADP-ribosylation factor-like 4 /DB XREF-gi:5031602 /UG-Hs.201672 ADP-ribosylation factor-like 4 /FL=gb:U73960.1 gb:NM_005738.1
212052_s_at	Consensus includes gb:AB014576.1 /DEF=Homo sapiens mRNA for KIAA0676 protein, partial cds. /FEA-mRNA /GEN=KIAA0676 /PROD=KIAA0676 protein /DB XREF-gi:3327165 /UG-Hs.155829 KIAA0676 protein

202565_s_at	gb:NM_003174.2 / DBF-Homo sapiens supervillin (SVIL), transcript variant 1, mRNA. / FEA=mrna / GEN=SVIL / PROD=supervillin, isoform 1 / DB XREF=gi:11496980 / UG=Hs.194567 supervillin / FL=gb:NM_003174.2 gb:AF051850.1 gb:AF051851.1
221524_s_at	gb:AF272036.1 / DEF-Homo sapiens Rag D mRNA, complete cds. / FEA=mrna / PROD=Rag D / DB XREF=gi:11181619 / UG=Hs.238679 Rag D protein / FL=gb:NM_021244.1 gb:AF272036.1 gb:BC003088.1
218037_at	gb:NM_024293.1 / DEF-Homo sapiens hypothetical protein MGC3035 / DB XREF=gi:13236511 / UG=Hs.22412 hypothetical protein MGC3035 / FL=gb:AL136758.1 gb:BC002420.1 gb:NM_024293.1
214107_x_at	Consensus includes gb:AW340850 / FEA=EST / DB XREF=gi:6837476 / DB XREF=est:31f01.x1 / CLONE=IMAGE:2761753 / UG=Hs.326350 Homo sapiens cDNA FLJ11822 fis, clone HEMBA1006485, highly similar to PUROMYCIN-SENSITIVE AMINOPEPTIDASE (EC 3.4.11.-)
210184_at	gb:M81695.1 / DEF-H. sapiens leukocyte adhesion glycoprotein p150, 95 mRNA, complete cds. / FEA=mrna / GEN=ITGAX / DB XREF=gi:487829 / UG=Hs.51077 Integrin, alpha X (antigen CD11c (p150), alpha polypeptide) / FL=gb:M81695.1 gb:NM_000887.2
209107_x_at	gb:U19179.1 / DEF-Human (Hln-2) mRNA, complete cds. / FEA=mrna / GEN=Hln-2 / DB XREF=gi:726037 / UG=Hs.74002 nuclear receptor coactivator 1 / FL=gb:U19179.1
208749_x_at	gb:AF085357.1 / DEF-Homo sapiens flotillin mRNA, complete cds. / FEA=mrna / PROD=Flotillin / DB XREF=gi:5114048 / UG=Hs.179986 flotillin 1 / FL=gb:BC001146.1 gb:AF085357.1 gb:AF089750.2 gb:NM_005803.2
212561_at	Consensus includes gb:AA349595 / FEA=EST / DB XREF=gi:2001934 / DB XREF=est:EST56429 / UG=Hs.26797 KIAA1091 protein
212470_at	Consensus includes gb:AB011088.1 / DEF-Homo sapiens mRNA for KIAA0516 protein, partial cds. / FEA=mrna / GEN=KIAA0516 / PROD=KIAA0516 protein / DB XREF=gi:3043555 / UG=Hs.129872 sperm associated antigen 9
214937_x_at	Consensus includes gb:AI924817 / FEA=EST / DB XREF=gi:5660781 / DB XREF=est:wn23c11.x1 / CLONE=IMAGE:2446292 / UG=Hs.75737 pericentriolar material 1
201783_s_at	gb:NM_021975.1 / DEF-Homo sapiens v-rel avian reticuloendotheliosis viral oncogene homolog A (nuclear factor of kappa light polypeptide gene enhancer in B-cells 3 (p65)) (REIA), mRNA. / FEA=mrna / GEN=REIA / PROD=v-rel avian reticuloendotheliosis viral oncogene homolog A (nuclear factor of kappa light polypeptide gene enhancer in B-cells 3 (p65)) / DB XREF=gi:11496238 / UG=Hs.75569 v-rel avian reticuloendotheliosis viral oncogene homolog A (nuclear factor of kappa light polypeptide gene enhancer in B-cells 3 (p65)) / FL=gb:NM_021975.1 gb:LI9067.1
202010_s_at	gb:NM_021188.1 / DEF-Homo sapiens clones 23667 and 23775 zinc finger protein (LOC57862), mRNA. / FEA=mrna / GEN=LOC57862 / PROD=Clones 23667 and 23775 zinc finger protein / DB XREF=gi:10863994 / UG=Hs.7137 clones 23667 and 23775 zinc finger protein / FL=gb:NM_021188.1 gb:U90919.1
201601_x_at	gb:NM_003641.1 / DEF-Homo sapiens interferon induced transmembrane protein 1 (9-27) (IFITM1), mRNA. / FEA=mrna / GEN=IFITM1 / PROD=Interferon induced transmembrane protein 1 (9-27) / DB XREF=gi:4504580 / UG=Hs.146360 interferon induced transmembrane protein 1 (9-27) / FL=gb:BC000897.1 gb:J04164.1 gb:NM_003641.1
203266_s_at	gb:NM_003010.1 / DEF-Homo sapiens mitogen-activated protein kinase kinase 4 (MAP2K4), mRNA. / FEA=mrna / GEN=MAP2K4 / PROD=mitogen-activated protein kinase kinase 4 / DB XREF=gi:4506888 / UG=Hs.75217 mitogen-activated protein kinase kinase 4 / FL=gb:NM_003010.1 gb:U17743.1
219863_at	gb:NM_016323.1 / DEF-Homo sapiens cyclin-E binding protein 1 (LOC51191), mRNA. / FEA=mrna / GEN=LOC51191 / PROD=Cyclin-E binding protein 1 / DB XREF=gi:7705930 / UG=Hs.26663 cyclin-E binding protein 1 / FL=gb:AB027289.1 gb:NM_016323.1
212322_at	Consensus includes gb:BE99972 / FEA=EST / DB XREF=gi:10700248 / DB XREF=est:7h15b02.x1 / CLONE=IMAGE:3316011 / UG=Hs.186613 sphingosine-1-phosphate lyase 1 / FL=gb:AF144638.1
204206_at	gb:NM_020310.1 / DEF-Homo sapiens MAX binding protein (MNT), mRNA. / FEA=mrna / GEN=MNT / PROD=MAX binding protein / DB XREF=gi:9945317 / UG=Hs.25497 MAX binding protein / FL=gb:NM_020310.1
203278_s_at	gb:NM_016621.1 / DEF-Homo sapiens hypothetical protein (LOC51317), mRNA. / FEA=mrna / GEN=LOC51317 / PROD=hypothetical protein / DB XREF=gi:7706159 / UG=Hs.106826 KIAA1696 protein / FL=gb:AF208848.1 gb:NM_016621.1
206637_at	gb:NM_014879.1 / DEF-Homo sapiens KIAA0001 gene product; putative G-protein-coupled receptor; G protein coupled receptor for UDP-glucose (KIAA0001), mRNA. / FEA=mrna / GEN=KIAA0001 / PROD=KIAA0001 gene product; putative G-protein-coupled receptor; G protein coupled receptor for UDP-glucose / DB XREF=gi:7661847 / UG=Hs.2465 KIAA0001 gene product; putative G-protein-coupled receptor; G protein coupled receptor for UDP-glucose / FL=gb:U13626.1 gb:NM_014879.1
218924_s_at	gb:NM_004388.1 / DEF-Homo sapiens chitobiose, di-N-acetyl- (CTBS), mRNA. / FEA=mrna / GEN=CTBS / PROD=chitobiose, di-N-acetyl- / DB XREF=gi:4758091 / UG=Hs.135578 chitobiose, di-N-acetyl- / FL=gb:H95767.1 gb:NM_004388.1

Tabelle 3: Gene aus Clusteranalyse 3

Affymetrix-interne Bezeichnung	Beschreibung der Sequenz in der GeneBank Datenbank
36711_at	Cluster Incl. AL021977:bk447C4.1 (novel MAF (v-maf musculoaponeurotic fibrosarcoma (avian) oncogene family, protein F) protein) / cds=(0,494) / gb=AL021977 / gi=4914526 / ug=Hs.51305 / len=2128
210845_s_at	gb:U08839.1 / DEF=Human urokinase-type plasminogen activator receptor mRNA, complete cds. / FEA=mRNA / PROD=urokinase-type plasminogen activator receptor / DB_XREF=gi:517197 / UG=Hs.179657 plasminogen activator, urokinase receptor / FL=gb:U08839.1
202643_s_at	Consensus includes gb:AI738896 / FEA=EST / DB_XREF=gi:5100877 / DB_XREF=est:w22902.x1 / CLONE=IMAGE:2391026 / UG=Hs.211600 tumor necrosis factor, alpha-induced protein 3 / FL=gb:M59465.1 gb:NM 006290.1
205476_at	gb:NM 004591.1 / DEF=Homo sapiens small inducible cytokine subfamily A (Cys-Cys), member 20 (SCYA20), mRNA. / FEA=mRNA / GEN=SCYA20 / PROD=small inducible cytokine subfamily A (Cys-Cys), member 20 / DB_XREF=gi:4759075 / UG=Hs.75498 small inducible cytokine subfamily A (Cys-Cys), member 20 / FL=gb:U64197.1 gb:U77035.1 gb:D86955.1 gb:NM 004591.1
205419_at	gb:NM 004951.1 / DEF=Homo sapiens Epstein-Barr virus induced gene 2 (lymphocyte-specific G protein-coupled receptor) (EBI2), mRNA. / FEA=mRNA / GEN=EBI2 / PROD=Epstein-Barr virus induced gene 2 (lymphocyte-specific G protein-coupled receptor) / DB_XREF=gi:4826705 / UG=Hs.784 Epstein-Barr virus induced gene 2 (lymphocyte-specific G protein-coupled receptor) / FL=gb:U08177.1 gb:NM 004951.1
209795_at	gb:U07555.1 / DEF=Homo sapiens early activation antigen CD69 mRNA, complete cds. / FEA=mRNA / PROD=early activation antigen CD69 / DB_XREF=gi:291897 / UG=Hs.82401 CD69 antigen (p60, early T-cell activation antigen) / FL=gb:U07555.1 gb:NM 001781.1
205767_at	gb:NM 001432.1 / DEF=Homo sapiens epiregulin (EREG), mRNA. / FEA=mRNA / GEN=EREG / PROD=epiregulin precursor / DB_XREF=gi:4557566 / UG=Hs.115263 epiregulin / FL=gb:D30783.1 gb:NM 001432.1
203821_at	gb:NM 001945.1 / DEF=Homo sapiens diphtheria toxin receptor (heparin-binding epidermal growth factor-like growth factor) (DTR), mRNA. / FEA=mRNA / GEN=DTR / PROD=diphtheria toxin receptor (heparin-binding epidermal growth factor-like growth factor) / DB_XREF=gi:4503412 / UG=Hs.799 diphtheria toxin receptor (heparin-binding epidermal growth factor-like growth factor) / FL=gb:M60278.1 gb:NM 001945.1
211924_s_at	gb:AY029180.1 / DEF=Homo sapiens soluble urokinase plasminogen activator receptor precursor (SUPAR) mRNA, complete cds. / FEA=CDs / GEN=SUPAR / PROD=soluble urokinase plasminogen activator receptor precursor / DB_XREF=gi:13641308 / FL=gb:AY029180.1
205403_at	gb:NM 004633.1 / DEF=Homo sapiens interleukin 1 receptor, type II (IL1R2), mRNA. / FEA=mRNA / GEN=IL1R2 / PROD=interleukin 1 receptor, type II / DB_XREF=gi:4758597 / UG=Hs.25333 interleukin 1 receptor, type II / FL=gb:U74649.1 gb:NM 004633.1
204351_at	gb:NM 005980.1 / DEF=Homo sapiens S100 calcium-binding protein P (S100P), mRNA. / FEA=mRNA / GEN=S100P / PROD=S100 calcium-binding protein P / DB_XREF=gi:5174662 / UG=Hs.2962 S100 calcium-binding protein P / FL=gb:NM 005980.1
206115_at	gb:NM 004430.1 / DEF=Homo sapiens early growth response 3 (EGR3), mRNA. / FEA=mRNA / GEN=EGR3 / PROD=early growth response 3 / DB_XREF=gi:4758251 / UG=Hs.74088 early growth response 3 / FL=gb:NM 004430.1
204103_at	gb:NM 002984.1 / DEF=Homo sapiens small inducible cytokine A4 (homologous to mouse Mip-1b) (SCYA4), mRNA. / FEA=mRNA / GEN=SCYA4 / PROD=small inducible cytokine A4 (homologous to mouse Mip-1b) / DB_XREF=gi:4506844 / UG=Hs.75703 small inducible cytokine A4 (homologous to mouse Mip-1b) / FL=gb:J04130.1 gb:NM 002984.1 gb:M23502.1 gb:M25316.1
206522_at	gb:NM 004668.1 / DEF=Homo sapiens maltase-glucoamylase (alpha-glucosidase) (MGAM), mRNA. / FEA=mRNA / GEN=MGAM / PROD=alpha-glucosidase / DB_XREF=gi:4758711 / UG=Hs.122785 maltase-glucoamylase (alpha-glucosidase) / FL=gb:AF016833.1 gb:NM 004668.1
202147_s_at	gb:NM 001550.1 / DEF=Homo sapiens interferon-related developmental regulator 1 (IFRD1), mRNA. / FEA=mRNA / GEN=IFRD1 / PROD=interferon-related developmental regulator 1 / DB_XREF=gi:4504606 / UG=Hs.7879 interferon-related developmental regulator 1 / FL=gb:BC001272.1 gb:NM 001550.1
206515_at	gb:NM 000896.1 / DEF=Homo sapiens cytochrome P450, subfamily IVF, polypeptide 3 (leukotriene B4 omega hydroxylase) (CYP4F3), mRNA. / FEA=mRNA / GEN=CYP4F3 / PROD=cytochrome P450, subfamily IVF, polypeptide 3 (leukotriene B4 omega hydroxylase) / DB_XREF=gi:4503240 / UG=Hs.106242 cytochrome P450, subfamily IVF, polypeptide 3 (leukotriene B4 omega hydroxylase) / FL=gb:AB002454.1 gb:D12620.1 gb:NM 000896.1
204614_at	gb:NM 002575.1 / DEF=Homo sapiens serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 2 (SERPINB2), mRNA. / FEA=mRNA / GEN=SERPINB2 / PROD=serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 2 / DB_XREF=gi:4505594 /

	UG-Hs.75716 serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 2 / FL=gb:J02685.1 gb:J03603.1
209959_at	gb:M18082.1 gb:NM 002575.1 gb:D12767.1 /DEF=Human mitogen induced nuclear orphan receptor (MINOR) mRNA, complete cds. /FEA=mrna /GEN=MINOR / PROD=mitogen induced nuclear orphan receptor /DB_XREF=gi:924281 /UG-Hs.80561 nuclear receptor subfamily 4, group A, member 3 / FL=gb:U12767.1
215078_at	Consensus includes gb:AL050388.1 /DEF=Homo sapiens mRNA; cDNA DKFZp564M2422 (from clone DKFZp564M2422); partial cds. / FEA=mrna /GEN=DKFZp564M2422 /PROD=hypothetical protein /DB_XREF=gi:4914612 /UG-Hs.306320 Homo sapiens mRNA; cDNA DKFZp564M2422 (from clone DKFZp564M2422); partial cds
201890_at	Consensus includes gb:BE966236 /FEA=EST /DB_XREF=gi:11771437 /DB_XREF=est:601660172R1 /CLONE=IMAGE:3905920 /UG-Hs.75319 ribonucleotide reductase M2 polypeptide /FL=gb:NM 001034.1
201489_at	gb:BC005020.1 /DEF=Homo sapiens, peptidylprolyl isomerase F (cyclophilin F), Clone MGC:11022, mRNA, complete cds. /FEA=mrna / PROD=peptidylprolyl isomerase F (cyclophilin F) /DB_XREF=gi:13477126 /UG-Hs.173125 peptidylprolyl isomerase F (cyclophilin F) / FL=gb:BC005020.1 gb:M80254.1 gb:NM 005729.1
203888_at	gb:NM 000361.1 /DEF=Homo sapiens thrombomodulin (THBD), mRNA. /FEA=mrna /GEN=THBD /PROD=thrombomodulin /DB_XREF=gi:4507482 / UG-Hs.2030 thrombomodulin /FL=gb:M16552.1 gb:NM 000361.1
218723_s_at	gb:NM 014059.1 /DEF=Homo sapiens RGC32 protein (RGC32), mRNA. /FEA=mrna /GEN=RGC32 /PROD=RGC32 protein /DB_XREF=gi:7662650 / UG-Hs.76640 RGC32 protein /FL=gb:AF036549.1 gb:NM 014059.1
206834_at	gb:NM 000519.2 /DEF=Homo sapiens hemoglobin, delta (HBD), mRNA. /FEA=mrna /GEN=ADM /PROD=adrenomedullin /DB_XREF=gi:4501944 / UG-Hs.36977 hemoglobin, delta /FL=gb:NM 000519.2
205479_s_at	gb:NM 002658.1 /DEF=Homo sapiens plasminogen activator, urokinase (PLAU), mRNA. /FEA=mrna /GEN=PLAU /PROD=plasminogen activator, urokinase /DB_XREF=gi:4505862 /UG-Hs.77274 plasminogen activator, urokinase /FL=gb:M15476.1 gb:NM 002658.1
202912_at	gb:NM 001124.1 /DEF=Homo sapiens adrenomedullin (ADM), mRNA. /FEA=mrna /GEN=ADM /PROD=adrenomedullin /DB_XREF=gi:4501944 / UG-Hs.394 adrenomedullin /FL=gb:NM 001124.1 gb:D14874.1
208869_s_at	gb:AF087847.1 /DEF=Homo sapiens GABA-A receptor-associated protein like 1 (GABARAPL1) mRNA, complete cds. /FEA=mrna / GEN=GABARAPL1 /PROD=GABA-A receptor-associated protein like 1 /DB_XREF=gi:13375570 /UG-Hs.282654 Homo sapiens mRNA; cDNA DKFZp564N1272 (from clone DKFZp564N1272); complete cds /FL=gb:AL136676.1 gb:AF087847.1
202193_at	gb:NM 005569.2 /DEF=Homo sapiens LIM domain kinase 2 (LIMK2), transcript variant 2a, mRNA. /FEA=mrna /GEN=LIMK2 / PROD=LIM domain kinase 2 isoform 2a /DB_XREF=gi:8051619 /UG-Hs.278027 LIM domain kinase 2 /FL=gb:D45906.1 gb:NM 005569.2
214696_at	Consensus includes gb:AF070569.1 /DEF=Homo sapiens clone 24659 mRNA sequence. /FEA=mrna /DB_XREF=gi:3387938 /UG-Hs.29206 Homo sapiens clone 24659 mRNA sequence
38037_at	Cluster Incl. M60278:Human heparin-binding EGF-like growth factor mRNA, complete cds /cds=(261,887) /gb=M60278 /gi=183866 / ug=Hs.799 /len=2342
212723_at	Consensus includes gb:AK021780.1 /DEF=Homo sapiens cDNA FLJ11718 fls, clone HEMBA1005252, highly similar to Homo sapiens mRNA for KIA0585 protein. /FEA=mrna /DB_XREF=gi:10433034 /UG-Hs.72660 phosphatidylserine receptor
207802_at	gb:NM 006061.1 /DEF=Homo sapiens specific granule protein (28 kDa); cysteine-rich secretory protein-3 (SGP28), mRNA. /FEA=mrna / GEN=SGP28 /PROD=specific granule protein (28 kDa); cysteine-rich secretory protein-3 /DB_XREF=gi:5174674 /UG-Hs.54431 specific granule protein (28 kDa); cysteine-rich secretory protein-3 /FL=gb:NM 006061.1
209967_s_at	gb:D14826.1 /DEF=Human mRNA for hCREM (cyclic AMP-responsive element modulator) type 2 protein, complete cds. /FEA=mrna / GEN=hCREM-2; hCREM-2; hCREM-2 /PROD=hCREM 2beta-b protein; hCREM 2beta-a protein; hCREM 2beta-b protein; hCREM 2alpha-a protein /DB_XREF=gi:532036 /UG-Hs.155924 cAMP responsive element modulator /FL=gb:AF069065.1 gb:D14826.1
210119_at	gb:U73191.1 /DEF=Human inward rectifier potassium channel (Kir1.3), complete cds. /FEA=mrna /GEN=Kir1.3 /PROD=inward rectifier potassium channel /DB_XREF=gi:1765984 /UG-Hs.17287 potassium inwardly-rectifying channel, subfamily J, member 15 / FL=gb:U73191.1 gb:NM 002243.1
203435_s_at	gb:NM 007287.1 /DEF=Homo sapiens membrane metallo-endopeptidase (neutral endopeptidase, enkephalinase, CALLA, CD10) (MME), transcript variant 1b1s, mRNA. /FEA=mrna /GEN=MME /PROD=membrane metallo-endopeptidase /DB_XREF=gi:6042199 /UG-Hs.1298 membrane metallo-endopeptidase (neutral endopeptidase, enkephalinase, CALLA, CD10) /FL=gb:J03779.1 gb:NM 007287.1 gb:NM 007288.1
213515_x_at	Consensus includes gb:AL133353 /FEA=EST /DB_XREF=est:HA1957 /UG-Hs.298161 myosin, light polypeptide 4, alkali; atrial, embryonic
209545_s_at	gb:AF064824.1 /DEF=Homo sapiens CARD-containing ICE associated kinase mRNA, complete cds. /FEA=mrna /PROD=CARD-containing ICE associated kinase /DB_XREF=gi:3290171 /UG-Hs.103755 receptor-interacting serine-threonine kinase 2 /FL=gb:BC004553.1
212531_at	gb:AF027706.1 gb:AF064824.1 gb:AF078530.1 gb:NM 003821.1 Consensus includes gb:NM 005564.1 /DEF=Homo sapiens lipocalin 2 (oncogene 24p3) (LCN2), mRNA. /FEA=cds /GEN=LCN2 / PROD=lipocalin 2 (oncogene 24p3) /DB_XREF=gi:5031852 /UG-Hs.204238 lipocalin 2 (oncogene 24p3) /FL=gb:NM 005564.1

208470_s_at	gb:NM 020995.1 / DEF=Homo sapiens haptoglobin-related protein (HPR), mRNA. / FEA=CDS / GEN=HPR / PROD=haptoglobin-related protein / DB XREF=gi:10337588 / UG=Hs.328822 haptoglobin-related protein / FL=gb:NM 020995.1
200733_s_at	gb:U48296.1 / DEF=Homo sapiens protein tyrosine phosphatase PTPCAX1 (hPTPCAX1) mRNA, complete cds. / FEA=mRNA / GEN=hPTPCAX1 / PROD=protein tyrosine phosphatase PTPCAX1 / DB XREF=gi:177754 / UG=Hs.22777 protein tyrosine phosphatase type IVA, member 1 / FL=gb:U48296.1 gb:NM 003463.1
211372_s_at	gb:U64094.1 / DEF=Human soluble type II interleukin-1 receptor mRNA, complete cds. / FEA=mRNA / PROD=soluble type II interleukin-1 receptor / DB XREF=gi:148065 / UG=Hs.25333 interleukin 1 receptor, type II / FL=gb:U64094.1
204794_at	gb:NM 004418.2 / DEF=Homo sapiens dual specificity phosphatase 2 (DUSP2), mRNA. / FEA=mRNA / GEN=DUSP2 / PROD=dual specificity phosphatase 2 / DB XREF=gi:12707563 / UG=Hs.1183 dual specificity phosphatase 2 / FL=gb:NM 004418.2 gb:L11329.1
206177_s_at	gb:NM 000045.2 / DEF=Homo sapiens arginase, liver (ARG1), mRNA. / FEA=mRNA / GEN=ARG1 / PROD=arginase, type I / DB XREF=gi:10947138 / UG=Hs.289057 arginase, liver / FL=gb:NM 000045.2 gb:M14502.1
205239_at	gb:NM 001657.1 / DEF=Homo sapiens amphiregulin (schwannoma-derived growth factor) (AREG), mRNA. / FEA=mRNA / GEN=AREG / PROD=amphiregulin (schwannoma-derived growth factor) / DB XREF=gi:4502198 / UG=Hs.270833 amphiregulin (schwannoma-derived growth factor) / FL=gb:M30704.1 gb:NM 001657.1
207094_at	gb:NM 000634.1 / DEF=Homo sapiens interleukin 8 receptor, alpha (IL8RA), mRNA. / FEA=mRNA / GEN=IL8RA / PROD=interleukin 8 receptor, alpha / DB XREF=gi:4504680 / UG=Hs.194778 interleukin 8 receptor, alpha / FL=gb:M68932.1 gb:NM 000634.1 gb:L19591.1
200776_s_at	Consensus includes gb:AL518328 / FEA=EST / DB XREF=gi:12781821 / DB XREF=est:AL518328 / CLONE=CSODA009YK18 (3 prime) / UG=Hs.155291
215009_s_at	K1AA0005 gene product / FL=gb:DI3630.1 gb:NM 014670.1
211302_s_at	Consensus includes gb:U92014.1 / DEF=Human clone 121711 defective mariner transposon Hsmar2 mRNA sequence. / FEA=mRNA / DB XREF=gi:2052456 / UG=Hs.153527 Homo sapiens pTM5 mariner-like transposon mRNA, partial sequence
210512_s_at	gb:L20966.1 / DEF=Human phosphodiesterase mRNA, complete cds. / FEA=mRNA / PROD=phosphodiesterase / DB XREF=gi:347121 / UG=Hs.188 phosphodiesterase 4B, cAMP-specific (dunce (Drosophila)-homolog phosphodiesterase E4) / FL=gb:L20966.1
210512_s_at	gb:AF022375.1 / DEF=Homo sapiens vascular endothelial growth factor mRNA, complete cds. / FEA=mRNA / PROD=vascular endothelial growth factor / DB XREF=gi:3719220 / UG=Hs.73793 vascular endothelial growth factor / FL=gb:M32977.1 gb:AF022375.1
212577_at	gb:NM 003376.1 gb:AB021221.1 gb:AF091352.1
212577_at	Consensus includes gb:AA688754 / FEA=EST / DB XREF=gi:2964199 / DB XREF=est:ak52e09.s1 / CLONE=IMAGE:1409608 / UG=Hs.8118 K1RA0650 protein
214866_at	Consensus includes gb:X74039.1 / DEF=H. sapiens mRNA for urokinase plasminogen activator receptor. / FEA=mRNA / PROD=urokinase plasminogen activator receptor / DB XREF=gi:456192 / UG=Hs.179657 plasminogen activator, urokinase receptor
219228_at	gb:NM 018555.2 / DEF=Homo sapiens C2H2-like zinc finger protein (ZNF361), mRNA. / FEA=mRNA / GEN=ZNF361 / PROD=C2H2-like zinc finger protein / DB XREF=gi:10092612 / UG=Hs.147644 zinc finger protein 331 / FL=gb:AF251515.2 gb:NM 018555.2 gb:AF272148.1
201574_at	gb:NM 004730.1 / DEF=Homo sapiens eukaryotic translation termination factor 1 (ETTF1), mRNA. / FEA=mRNA / GEN=ETTF1 / PROD=eukaryotic translation termination factor 1 / DB XREF=gi:4759033 / UG=Hs.77324 eukaryotic translation termination factor 1 / FL=gb:U90176.1 gb:M75715.1 gb:NM 004730.1
209498_at	Consensus includes gb:X16354.1 / DEF=Human mRNA for transmembrane carcinoembryonic antigen BGPa (formerly TM1-CEA). / FEA=mRNA / PROD=TM1-CEA preprotein / DB XREF=gi:37197 / UG=Hs.50964 carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein) / FL=gb:J03858.1
207630_s_at	gb:NM 001881.1 / DEF=Homo sapiens cAMP responsive element modulator (CREM), mRNA. / FEA=mRNA / GEN=CREM / PROD=cAMP responsive element modulator / DB XREF=gi:4503038 / UG=Hs.155924 cAMP responsive element modulator / FL=gb:NM 001881.1 gb:S68271.1
210873_x_at	gb:U03891.2 / DEF=Homo sapiens phorbolins I mRNA, complete cds. / FEA=mRNA / PROD=phorbolins I / DB XREF=gi:4895107 / UG=Hs.226307 phorbolins (similar to apolipoprotein B mRNA editing protein) / FL=gb:U03891.2
204419_x_at	gb:NM 000184.1 / DEF=Homo sapiens hemoglobin, gamma G (HBG2), mRNA. / FEA=mRNA / GEN=HBG2 / PROD=hemoglobin, gamma G / DB XREF=gi:6715606 / UG=Hs.283108 hemoglobin, gamma G / FL=gb:NM 000184.1
202988_s_at	gb:NM 002922.1 / DEF=Homo sapiens regulator of G-protein signalling 1 (RGS1), mRNA. / FEA=mRNA / GEN=RGS1 / PROD=regulator of G-protein signalling 1 / DB XREF=gi:4506514 / UG=Hs.75256 regulator of G-protein signalling 1 / FL=gb:NM 002922.1
209273_s_at	Consensus includes gb:BG387555 / FEA=EST / DB XREF=gi:13281001 / DB XREF=est:602412371f1 / CLONE=IMAGE:4521017 / UG=Hs.177776 hypothetical protein MGC4276 similar to CGB198 / FL=gb:AF284752.1 gb:BC002675.1
202693_s_at	Consensus includes gb:AW194730 / FEA=EST / DB XREF=gi:6473630 / DB XREF=est:xn43d11.x1 / CLONE=IMAGE:2696469 / UG=Hs.9075 serine/threonine kinase 17a (apoptosis-inducing) / FL=gb:AB011420.1 gb:NM 004760.1
205270_s_at	gb:NM 005565.2 / DEF=Homo sapiens lymphocyte cytosolic protein 2 (SH2 domain-containing leukocyte protein of 76kD) (LCP2), mRNA. / FEA=mRNA / GEN=LCP2 / PROD=lymphocyte cytosolic protein 2 / DB XREF=gi:7382491 / UG=Hs.2488 lymphocyte cytosolic protein 2 (SH2 domain-containing leukocyte protein of 76kD) / FL=gb:NM 005565.2 gb:U20158.1

202284_s_at	gb:NM_000389.1 /DEF=Homo sapiens cyclin-dependent kinase inhibitor 1A (p21, Cip1) (CDKN1A), mRNA. /FEA=mrna /GEN=CDKN1A / PROD=cyclin-dependent kinase inhibitor 1A (p21, Cip1) /DB_XREF=gi:11386202 /UG=Hs.179665 cyclin-dependent kinase inhibitor 1A (p21, Cip1) /FL=gb:NM_000389.1 gb:BC000275.1 gb:BC001935.1 gb:003106.1 gb:126165.1 gb:125610.1 gb:U09579.1
219471_at	gb:NM_025113.1 /DEF=Homo sapiens hypothetical protein FLJ21562 (FLJ21562), mRNA. /FEA=mrna /GEN=FLJ21562 /PROD=hypothetical protein FLJ21562 /DB_XREF=gi:13376686 /UG=Hs.288708 hypothetical protein FLJ21562 /FL=gb:NM_025113.1
208651_x_at	gb:M58664.1 /DEF=Homo sapiens CD24 signal transducer mRNA, complete cds. /FEA=mrna /PROD=signal transducer CD24 / DB_XREF=gi:180167 /UG=Hs.286124 CD24 antigen (small cell lung carcinoma cluster 4 antigen) /FL=gb:M58664.1 gb:L33930.1 gb:NM_013230.1
211434_s_at	gb:AF015524.1 /DEF=Homo sapiens putative chemokine receptor (CRAM-A) mRNA, complete cds. /FEA=mrna /GEN=CRAM-A / PROD=putative chemokine receptor /DB_XREF=gi:3550066 /UG=Hs.302043 chemokine (C-C motif) receptor-like 2 /FL=gb:AF015524.1
204285_s_at	Consensus includes gb:AI857639 /FEA=EST /DB_XREF=gi:5511255 /DB_XREF=est:wk95g09.x1 /CLONE=IMAGE:2423200 /UG=Hs.96 phorbol-12-myristate-13-acetate-induced protein 1 /FL=gb:NM_021127.1
221824_s_at	Consensus includes gb:AA770170 /FEA=EST /DB_XREF=gi:2821408 /DB_XREF=est:ah84d09.s1 /CLONE=1322321 /UG=Hs.288156 Homo sapiens cDNA: FLJ21819 fis. clone HEP01185
219081_at	gb:NM_024668.1 /DEF=Homo sapiens hypothetical protein FLJ20288 (FLJ20288), mRNA. /FEA=mrna /GEN=FLJ20288 /PROD=hypothetical protein FLJ211979 /DB_XREF=gi:13386461 /UG=Hs.84045 hypothetical protein FLJ20288 /FL=gb:BC004457.1 gb:NM_024668.1
220528_at	gb:NM_018399.1 /DEF=Homo sapiens VNN3 protein (HSA238982), mRNA. /FEA=mrna /GEN=HSA238982 /PROD=VNN3 protein / DB_XREF=gi:9055235 /UG=Hs.183636 VNN3 protein /FL=gb:NM_018399.1
205896_at	gb:NM_003059.1 /DEF=Homo sapiens solute carrier family 22 (organic cation transporter), member 4 (SLC22A4), mRNA. / FEA=mrna /GEN=SLC22A4 /PROD=solute carrier family 22 (organic cation transporter), member 4 /DB_XREF=gi:4507002 / UG=Hs.77239 solute carrier family 22 (organic cation transporter), member 4 /FL=gb:AB007448.1 gb:NM_003059.1
211445_x_at	gb:AF315951.1 /DEF=Homo sapiens FKSG17 (FKSG17) mRNA, complete cds. /FEA=mrna /GEN=FKSG17 /PROD=FKSG17 /DB_XREF=gi:12276119 / UG=Hs.307057 Homo sapiens FKSG17 (FKSG17) mRNA, complete cds /FL=gb:AF315951.1
204286_s_at	gb:NM_021127.1 /DEF=Homo sapiens phorbol-12-myristate-13-acetate-induced protein 1 (PMAIP1), mRNA. /FEA=mrna /GEN=PMAIP1 / PROD=phorbol-12-myristate-13-acetate-induced protein1 /DB_XREF=gi:10863922 /UG=Hs.96 phorbol-12-myristate-13-acetate-induced protein 1 /FL=gb:NM_021127.1
202503_s_at	gb:NM_014736.1 /DEF=Homo sapiens KIAA0101 gene product (KIAA0101), mRNA. /FEA=mrna /GEN=KIAA0101 /PROD=KIAA0101 gene product / DB_XREF=gi:7661905 /UG=Hs.81892 KIAA0101 gene product /FL=gb:D14657.1 gb:NM_014736.1
211560_s_at	gb:AF130113.1 /DEF=Homo sapiens clone FLB929 PROD3399 mRNA, complete cds. /FEA=mrna /PROD=PROD3399 /DB_XREF=gi:11493529 / UG=Hs.79103 cytochrome b5 outer mitochondrial membrane precursor /FL=gb:AF130113.1
209945_s_at	gb:BC000251.1 /DEF=Homo sapiens, Similar to glycogen synthase kinase 3 beta, clone MGC:1736, mRNA, complete cds. / FEA=mrna /PROD=Similar to glycogen synthase kinase 3 beta /DB_XREF=gi:12652980 /UG=Hs.78802 glycogen synthase kinase 3 beta / FL=gb:BC000251.1
217997_at	Consensus includes gb:AI795908 /FEA=EST /DB_XREF=gi:5361371 /DB_XREF=est:wh40a05.x1 /CLONE=IMAGE:2383184 /UG=Hs.82101 pieckstrin homology-like domain, family A, member 1 /FL=gb:NM_007350.1
203757_s_at	gb:BC005008.1 /DEF=Homo sapiens, carcinoembryonic antigen-related cell adhesion molecule 6 (non-specific cross reacting antigen), clone MGC:10467, mRNA, complete cds. /FEA=mrna /PROD=carcinoembryonic antigen-related cell adhesion molecule 6 (non-specific cross reacting antigen) /DB_XREF=gi:13477106 /UG=Hs.73848 carcinoembryonic antigen-related cell adhesion molecule 6 (non-specific cross reacting antigen) /FL=gb:BC005008.1 gb:M18216.1 gb:M29541.1 gb:NM_002483.1
205269_at	Consensus includes gb:AI123251 /FEA=EST /DB_XREF=gi:3539017 /DB_XREF=est:ga47g03.x1 /CLONE=IMAGE:1689940 /UG=Hs.2488 Lymphocyte cytosolic protein 2 (SH2 domain-containing leukocyte protein of 76kD) /FL=gb:NM_005565.2 gb:U20158.1
219049_at	gb:NM_018371.1 /DEF=Homo sapiens hypothetical protein FLJ11264 (FLJ11264), mRNA. /FEA=mrna /GEN=FLJ11264 /PROD=hypothetical protein FLJ11264 /DB_XREF=gi:8922959 /UG=Hs.11260 hypothetical protein FLJ11264 /FL=gb:NM_018371.1
209396_s_at	gb:M80927.1 /DEF=Human glycoprotein mRNA, complete cds. /FEA=mrna /PROD=glycoprotein /DB_XREF=gi:348911 /UG=Hs.75184 chitinase 3-like 1 (cartilage glycoprotein-39) /FL=gb:M80927.1 gb:NM_001215.1
202637_s_at	Consensus includes gb:AI608725 /FEA=EST /DB_XREF=gi:4617892 /DB_XREF=est:tw90b01.x1 /CLONE=IMAGE:2266921 /UG=Hs.168383 intercellular adhesion molecule 1 (CD54), human rhinovirus receptor /FL=gb:M24283.1 gb:J03132.1 gb:NM_000201.1
205557_at	gb:NM_001725.1 /DEF=Homo sapiens bactericidal/permeability-increasing protein (BPI), mRNA. /FEA=mrna /GEN=BPI /PROD=bactericidal/permeability-increasing protein precursor /DB_XREF=gi:4502446 /UG=Hs.89535 bactericidal/permeability-increasing protein /FL=gb:AF322588.1 gb:J04739.1 gb:NM_001725.1
207072_at	gb:NM_003853.1 /DEF=Homo sapiens interleukin 18 receptor accessory protein (IL18RAP), mRNA. /FEA=mrna /GEN=IL18RAP /PROD=interleukin 18 receptor accessory protein /DB_XREF=gi:4504656 /UG=Hs.158315 interleukin 18 receptor accessory protein /FL=gb:AF077346.1 gb:NM_003853.1

202498_s_at	Consensus includes gb:BE550486 /FEA-EST /DB_XREF=gi:9792178 /DB_XREF=est:7a27c01.x1 /CLONE=IMAGE:3219936 /UG=Hs.7594 solute carrier family 2 (facilitated glucose transporter), member 3 /FL=gb:M20681.1 gb:NM 006931.1
218739_at	gb:NM 016006.1 /DEF=Homo sapiens CGI-58 protein (LOC10399), mRNA. /FEA-mRNA /GEN=LOC10399 /PROD=CGI-58 protein /DB_XREF=gi:7705770 /UG=Hs.19385 CGI-58 protein /FL=gb:AF151816.1 gb:NM 016006.1
212722_s_at	Consensus includes gb:AK021780.1 /DEF=Homo sapiens cDNA FL11718 f1s, clone HEMBA1005252, highly similar to Homo sapiens mRNA for KIAA0585 protein. /FEA-mRNA /DB_XREF=gi:10433034 /UG=Hs.72660 phosphatidylserine receptor
212930_at	Consensus includes gb:AW576457 /FEA-EST /DB_XREF=gi:1047996 /DB_XREF=est:U1-BRQp-aji-a-01-0-UI.s1 /CLONE=IMAGE:3074568 /UG=Hs.20952 Homo sapiens clone 24411 mRNA sequence
200985_s_at	gb:NM 000611.1 /DEF=Homo sapiens CD59 antigen p18-20 (antigen identified by monoclonal antibodies 16.3A5, EJ16, EJ30, EL32 and G344) (CD59), mRNA. /FEA-mRNA /GEN=CD59 /PROD=CD59 antigen p18-20 (antigen identified by monoclonal antibodies 16.3A5, EJ16, EJ30, EL32 and G344) /DB_XREF=gi:10835164 /UG=Hs.119663 CD59 antigen p18-20
206026_s_at	(antigen identified by monoclonal antibodies 16.3A5, EJ16, EJ30, EL32 and G344) /FL=gb:NM 000611.1 gb:M34671.1 /gb:NM 007115.1 /DEF=Homo sapiens tumor necrosis factor, alpha-induced protein 6 (TNFAIP6), mRNA. /FEA-mRNA /GEN=TNFAIP6 /PROD=tumor necrosis factor, alpha-induced protein 6 /DB_XREF=gi:6005905
210740_s_at	/UG=Hs.29352 tumor necrosis factor, alpha-induced protein 6 /FL=gb:NM 007115.1
202333_s_at	gb:AF279372.1 /DEF=Homo sapiens inositol 1,3,4-trisphosphate 56-kinase mRNA, complete cds. /FEA-mRNA /PROD=inositol 1,3,4-trisphosphate 56-kinase /DB_XREF=gi:12006345 /UG=Hs.6453 inositol 1,3,4-trisphosphate 56 kinase /FL=gb:AF279372.1
201566_x_at	Consensus includes gb:AA877765 /FEA-EST /DB_XREF=gi:2986730 /DB_XREF=est:nr06f05.s1 /CLONE=IMAGE:1161057 /UG=Hs.811
44790_s_at	ubiquitin-conjugating enzyme E2B (RAD6 homolog) /FL=gb:M74525.1 gb:NM 003337.1
213891_s_at	gb:DL3891.1 /DEF=Human mRNA for Id-2H, complete cds. /FEA-mRNA /GEN=Id-2H /PROD=Id-2H /DB_XREF=gi:464183 /UG=Hs.180919
44790_s_at	Inhibitor of DNA binding 2, dominant negative helix-loop-helix protein /FL=gb:M97796.1 gb:NM 002166.1 gb:DL3891.1
213836_s_at	Cluster Incl. A1129310:qc48a05.x1 Homo sapiens cDNA, 3' end /clone=IMAGE-1712816 /clone_end=3 /gb=AL129310 /gi=3597824 /protein
205027_s_at	Consensus includes gb:AW052084 /FEA-EST /DB_XREF=gi:5914443 /DB_XREF=est:wy86f07.x1 /CLONE=IMAGE:2555461 /UG=Hs.279937 KIAA1001
207329_at	gb:NM 005204.1 /DEF=Homo sapiens mitogen-activated protein kinase kinase 8 (MAP3K8), mRNA. /FEA-mRNA /GEN=MAP3K8 /PROD=mitogen-activated protein kinase kinase 8 /FL=gb:DL4497.1 gb:NM 005204.1
217996_at	gb:NM 002424.1 /DEF=Homo sapiens matrix metalloproteinase 8 (neutrophil collagenase) (MMP8), mRNA. /FEA-mRNA /GEN=MMP8 /PROD=matrix metalloproteinase 8 /DB_XREF=gi:4505220
208632_at	Consensus includes gb:AA576961 /FEA-EST /DB_XREF=gi:2354435 /DB_XREF=est:nr82d08.s1 /CLONE=IMAGE:1074735 /UG=Hs.82101
206851_at	pleckstrin homology-like domain, family A, member 1 /FL=gb:NM 007350.1
203434_s_at	Consensus includes gb:AL578551 /FEA-EST /DB_XREF=gi:12942733 /DB_XREF=est:AL578551 /CLONE=CS0DK001YG01 (3 prime) /UG=Hs.5094 ring finger protein 10 /FL=gb:AB027196.1
216236_s_at	gb:NM 002935.1 /DEF=Homo sapiens ribonuclease, RNase A family, 3 (eosinophil cationic protein) (RNASE3), mRNA. /FEA-mRNA /GEN=RNASE3 /PROD=ribonuclease, RNase A family, 3 (eosinophil cationic protein) /DB_XREF=gi:4506550 /UG=Hs.73839 ribonuclease, RNase A family, 3 (eosinophil cationic protein) /FL=gb:NM 002935.1 gb:M28128.1
206342_x_at	Consensus includes gb:AI433463 /FEA-EST /DB_XREF=gi:4289355 /DB_XREF=est:ti65g11.x1 /CLONE=IMAGE:2136932 /UG=Hs.1298 membrane metallo-endopeptidase (neutrophil endopeptidase, enkephalinase, CALLA, CD10) /FL=gb:J03779.1 gb:NM 007287.1 gb:NM 007288.1
201329_s_at	Consensus includes gb:AL110298.1 /DEF=Homo sapiens mRNA, cDNA DKFZp564K1672 (from clone DKFZp564K1672); partial cds. /FEA-mRNA /GEN=DKFZp564K1672 /PROD=hypothetical protein /DB_XREF=gi:5817258 /UG=Hs.7594 solute carrier family 2 (facilitated glucose transporter), member 3
200731_s_at	gb:NM 006123.1 /DEF=Homo sapiens iduronate 2-sulfatase (Hunter syndrome) (IDS), transcript variant 2, mRNA. /FEA-mRNA /GEN=IDS /PROD=iduronate-2-sulfatase isoform b precursor /DB_XREF=gi:5360207 /UG=Hs.172458 iduronate 2-sulfatase (Hunter syndrome) /FL=gb:LA0586.1 gb:NM 006123.1
212508_at	gb:NM 005239.1 /DEF=Homo sapiens v-ets avian erythroblastosis virus E26 oncogene homolog 2 (ETS2), mRNA. /FEA-mRNA /GEN=ETS2 /PROD=v-ets avian erythroblastosis virus E26 oncogene homolog 2 /DB_XREF=gi:4885220 /UG=Hs.85146 v-ets avian erythroblastosis virus E26 oncogene homolog 2 /FL=gb:J04102.1 gb:NM 005239.1
	Consensus includes gb:AW165960 /FEA-EST /DB_XREF=gi:6397485 /DB_XREF=est:xf43a12.x1 /CLONE=IMAGE:2620798 /UG=Hs.227777 protein tyrosine phosphatase type IVA, member 1 /FL=gb:U48296.1 gb:NM 003463.1
	Consensus includes gb:AK024029.1 /DEF=Homo sapiens cDNA FLJ13967 f1s, clone Y79AAL001402, weakly similar to Homo sapiens paraneoplastic cancer-testis-brain antigen (M4) mRNA. /FEA-mRNA /DB_XREF=gi:10436287 /UG=Hs.24719 modulator of apoptosis 1 /

208868_s_at	FL-gb:AF305550.1 gb:NM_022151.1
204054_at	Consensus includes gb:BF125756 /FEA=EST /DB_XREF=gi:10964796 /DB_XREF=est:601763146F1 /CLONE=IMAGE:4026010 /UG=Hs.282654 Homo sapiens mRNA; cDNA DKEFp56AN1272 (from clone DKEFp56AN1272); complete cds /FL=gb:AL136676.1 gb:AF087847.1 gb:NM_000314.1 /DEF=Homo sapiens phosphatase and tensin homolog (mutated in multiple advanced cancers 1) (PTEN), mRNA. /FEA=mRNA /GEN=PTEN /PROD=phosphatase and tensin homolog (mutated in multiple advanced cancers 1) /DB_XREF=gi:4506248 /UG=Hs.10712 phosphatase and tensin homolog (mutated in multiple advanced cancers 1) /FL=gb:U92436.1 gb:U93051.1 gb:U96180.1 gb:NM_000314.1
212262_at	Consensus includes gb:AA149639 /FEA=EST /DB_XREF=gi:1720440 /DB_XREF=est:z139c06.s1 /CLONE=IMAGE:504298 /UG=Hs.15020 homolog of mouse quaking OKI (KH domain RNA binding protein) /FL=gb:AF142419.1 gb:AF142422.1
208785_s_at	Consensus includes gb:BE893893 /FEA=EST /DB_XREF=gi:1035516 /DB_XREF=est:601436260F1 /CLONE=IMAGE:3921446 /UG=Hs.121849 microtubule-associated proteins 1A1B light chain 3 /FL=gb:AF303888.1 gb:NM_022818.2 gb:AF183417.1
218660_at	gb:NM_003494.1 /DEF=Homo sapiens dysferlin, limb girdle muscular dystrophy 2B (autosomal recessive) (DYSF), mRNA. /FEA=mRNA /GEN=DYSF /PROD=dysferlin /DB_XREF=gi:4503430 /UG=Hs.143897 dysferlin, limb girdle muscular dystrophy 2B (autosomal recessive) /FL=gb:AF075575.1 gb:NM_003494.1
221920_s_at	Consensus includes gb:BE677761 /FEA=EST /DB_XREF=gi:10038376 /DB_XREF=est:7f59h05.x1 /CLONE=IMAGE:3299001 /UG=Hs.300496 mitochondrial solute carrier
211982_x_at	Consensus includes gb:AL546600 /FEA=EST /DB_XREF=gi:12879872 /DB_XREF=est:AL546600 /CLONE=CSOD1029YA23 (3 prime) /UG=Hs.70500 KIAA0370 protein
218647_s_at	gb:NM_024640.1 /DEF=Homo sapiens hypothetical protein FLJ23476 (FLJ23476), mRNA. /FEA=mRNA /GEN=FLJ23476 PROD=hypothetical protein FLJ23476 /DB_XREF=gi:13375875 /UG=Hs.46736 hypothetical protein FLJ23476 /FL=gb:NM_024640.1
206571_s_at	gb:NM_004834.1 /DEF=Homo sapiens mitogen-activated protein kinase kinase kinase 4 (MAP4K4), mRNA. /FEA=mRNA /GEN=MAP4K4 /PROD=mitogen-activated protein kinase kinase kinase 4 /DB_XREF=gi:4758523 /UG=Hs.3628 mitogen-activated protein kinase kinase kinase 4 /FL=gb:AF096300.1 gb:NM_004834.1
218332_at	gb:NM_018476.1 /DEF=Homo sapiens uncharacterized hypothetical protein HBEX2 (HBEX2), mRNA. /FEA=mRNA /GEN=HBEX2 /PROD=uncharacterized hypothetical protein HBEX2 /DB_XREF=gi:8923715 /UG=Hs.283719 uncharacterized hypothetical protein HBEX2 /FL=gb:AF220189.1 gb:NM_018476.1 gb:AF183416.1 gb:AF237783.1
207113_s_at	gb:NM_000594.1 /DEF=Homo sapiens tumor necrosis factor (TNF) superfamily, member 2) (TNF), mRNA. /FEA=mRNA /GEN=TNF /PROD=tumor necrosis factor (cachectin) /DB_XREF=gi:10835154 /UG=Hs.241570 tumor necrosis factor (TNF superfamily, member 2) /FL=gb:NM_000594.1
209388_at	gb:BC000927.1 /DEF=Homo sapiens, similar to poly (A) polymerase, clone MGC:5378, mRNA, complete cds. /FEA=mRNA /PROD=Similar to poly (A) polymerase /DB_XREF=gi:12654216 /UG=Hs.49007 poly(A) polymerase alpha /FL=gb:BC000927.1
207610_s_at	gb:NM_013447.1 /DEF=Homo sapiens egf-like module containing, mucin-like, hormone receptor-like sequence 2 (EMR2), mRNA. /FEA=mRNA /GEN=EMR2 /PROD=egf-like module containing, mucin-like, hormone receptor-like sequence 2 /DB_XREF=gi:7305024 /UG=Hs.137354 egf-like module containing, mucin-like, hormone receptor-like sequence 2 /FL=gb:AF114491.1 gb:NM_013447.1
204258_at	gb:NM_001270.1 /DEF=Homo sapiens chromodomain helicase DNA binding protein 1 (CHD1), mRNA. /FEA=mRNA /GEN=CHD1 /PROD=chromodomain helicase DNA binding protein 1 /DB_XREF=gi:4557446 /UG=Hs.22670 chromodomain helicase DNA binding protein 1 /FL=gb:AF006513.1 gb:NM_001270.1
200948_at	gb:NM_005439.1 /DEF=Homo sapiens myeloid leukemia factor 2 (MLF2), mRNA. /FEA=mRNA /GEN=MLF2 /PROD=myeloid leukemia factor 2 /DB_XREF=gi:4885486 /UG=Hs.79026 myeloid leukemia factor 2 /FL=gb:BC000898.1 gb:BC002340.1 gb:U57342.1 gb:AF070539.1 gb:NM_005439.1
211506_s_at	gb:AF043337.1 /DEF=Homo sapiens interleukin 8 C-terminal variant (IL8) mRNA, complete cds. /FEA=mRNA /GEN=IL8 /PROD=interleukin 8 C-terminal variant /DB_XREF=gi:12641914 /UG=Hs.624 interleukin 8 /FL=gb:AF043337.1
217966_s_at	gb:NM_022083.1 /DEF=Homo sapiens niban protein (NIBAN), mRNA. /FEA=mRNA /GEN=NIBAN /PROD=niban protein /DB_XREF=gi:11545796 /UG=Hs.48778 niban protein /FL=gb:AB050477.1 gb:NM_022083.1 gb:AF288391.1
214151_s_at	Consensus includes gb:AUI44243 /FEA=EST /DB_XREF=gi:11005764 /DB_XREF=est:AUI44243 /CLONE=HEMBA1001328 /UG=Hs.247118 phosphatidylinositol glycan, class B
211810_s_at	gb:D25284.1 /DEF=Human mRNA for alternative spliced product of galactocerebrosidase, complete cds. /FEA=CDS /PROD=alternative spliced product of galactocerebrosidase /DB_XREF=gi:457445 /UG=Hs.273 galactosylceramidase (Krabbe disease) /FL=gb:D25284.1
207890_s_at	gb:NM_022718.1 /DEF=Homo sapiens matrix metalloproteinase 25 (MMP25), transcript variant 2, mRNA. /FEA=mRNA /GEN=MMP25 /PROD=matrix metalloproteinase 25 preproprotein /DB_XREF=gi:13027808 /UG=Hs.198265 matrix metalloproteinase 25 /FL=gb:NM_022718.1

37028_at	Cluster Incl. U83981: Homo sapiens apoptosis associated protein (GADD34) mRNA, complete cds /cds=(222,2246) /gb=U83981 /gi=3258617 /ug=Hs.76556 /len=2331
40446_at	Cluster Incl. AL021366: C10K07210.4.1 (PHD finger protein 2) (isoform 2) /cds=(215,1918) /gb=AL021366 /gi=3169115 /ug=Hs.166204 /len=2260
219062_s_at	gb:NM_017742.1 /DEF=Homo sapiens hypothetical protein FLJ20281 (FLJ20281), mRNA. /FEA=mrna /GEN=FLJ20281 /PROD=hypothetical protein FLJ20281 /DB_XREF=gi:8923259 /UG=Hs.18800 hypothetical protein FLJ20281 /FL=gb:NM_017742.1
202158_s_at	gb:NM_006561.1 /DEF=Homo sapiens CUG triplet repeat, RNA-binding protein 2 (CUGBP2), mRNA. /FEA=mrna /GEN=CUGBP2 /PROD=CUG triplet repeat, RNA-binding protein 2 /DB_XREF=gi:5729815 /UG=Hs.211610 CUG triplet repeat, RNA-binding protein 2 /FL=gb:U69546.1 gb:AF036956.1 gb:AF090894.1 gb:NM_006561.1
60084_at	Cluster Incl. AI453099: t161e11.x1 Homo sapiens cDNA, 3' end /clone=IMAGE-2146028 /clone_end=3 /gb=AI453099 /gi=4307988 /ug=Hs.24668 /len=554
210142_x_at	gb:AF117234.1 /DEF=Homo sapiens flotillin mRNA, complete cds. /FEA=mrna /PROD=Flotillin /DB_XREF=gi:6563241 /UG=Hs.179986 Flotillin 1 /FL=gb:AF117234.1
204490_s_at	gb:M24915.1 /DEF=Human CD44 antigen, complete cds. /FEA=mrna /DB_XREF=gi:180196 /UG=Hs.169610 CD44 antigen (homolog function and Indian blood group system) /FL=gb:NM_000610.1 gb:U40373.1 gb:M59040.1 gb:M24915.1
203949_at	gb:NM_000250.1 /DEF=Homo sapiens myeloperoxidase (MPO), nuclear gene encoding mitochondrial protein, mRNA. /FEA=mrna /GEN=MPO /PROD=myeloperoxidase /DB_XREF=gi:4557758 /UG=Hs.1817 myeloperoxidase /FL=gb:M19507.1 gb:U02694.1 gb:NM_000250.1
219259_at	gb:NM_022367.1 /DEF=Homo sapiens hypothetical protein FLJ12287 similar to semaphorins (FLJ12287), mRNA. /FEA=mrna /GEN=FLJ12287 /PROD=hypothetical protein FLJ12287 similar to semaphorins /DB_XREF=gi:11641290 /UG=Hs.7634 hypothetical protein FLJ12287 similar to semaphorins /FL=gb:NM_022367.1 gb:AB029394.1
201751_at	gb:NM_014876.1 /DEF=Homo sapiens KIAA0063 gene product (KIAA0063), mRNA. /FEA=mrna /GEN=KIAA0063 /PROD=KIAA0063 gene product /DB_XREF=gi:7661887 /UG=Hs.3094 KIAA0063 gene product /FL=gb:D31884.1 gb:NM_014876.1
203153_at	gb:NM_001548.1 /DEF=Homo sapiens interferon-induced protein with tetratricopeptide repeats 1 (IFIT1), mRNA. /FEA=mrna /GEN=IFIT1 /PROD=interferon-induced protein with tetratricopeptide repeats 1 /DB_XREF=gi:4504584 /UG=Hs.20315 interferon-induced protein with tetratricopeptide repeats 1 /FL=gb:M24594.1 gb:NM_001548.1
210724_at	gb:AF239764.1 /DEF=Homo sapiens EGF-like module-containing mucin-like receptor EMR3 mRNA, complete cds. /FEA=mrna /PROD=EGF-like module-containing mucin-like receptor EMR3 /DB_XREF=gi:13183148 /UG=Hs.326777 Homo sapiens EGF-like module-containing mucin-like receptor EMR3 mRNA, complete cds /FL=gb:AF239764.1
202381_at	gb:NM_003816.1 /DEF=Homo sapiens a disintegrin and metalloproteinase domain 9 (meltrin gamma) (ADAM9), mRNA. /FEA=mrna /GEN=ADAM9 /PROD=a disintegrin and metalloproteinase domain 9 (meltrin gamma) /FL=gb:U41766.1 gb:NM_003816.1 /UG=Hs.2442 a disintegrin and metalloproteinase domain 9 (meltrin gamma) /FL=gb:U41766.1 gb:NM_003816.1
217824_at	Consensus includes gb:AW500009 /FEA=EST /DB_XREF=gi:7112213 /DB_XREF=est:U1-HF-BN0-aki-e-09-0-U1.r1 /CLONE=IMAGE:3077105 /UG=Hs.184325 CGI-76 protein /FL=gb:AF151834.1 gb:AF151039.1 gb:NM_016021.1
200984_s_at	Consensus includes gb:X1647.1 /DEF=Human mRNA for CD59, an IY-E-like protein regulating complement membrane attack. /FEA=mrna /PROD=precursor polypeptide (AA -25 to 103) /DB_XREF=gi:29805 /UG=Hs.119663 CD59 antigen p18-20 (antigen identified by monoclonal antibodies 16.3A5, EJ30, EJ32 and G344) /FL=gb:NM_000611.1 gb:M34671.1
219999_at	gb:NM_018621.1 /DEF=Homo sapiens hypothetical protein PRO2198 (PRO2198), mRNA. /FEA=mrna /GEN=PRO2198 /PROD=hypothetical protein PRO2198 /DB_XREF=gi:8924129 /UG=Hs.116459 hypothetical protein PRO2198 /FL=gb:AF116691.1 gb:NM_018621.1
212644_s_at	Consensus includes gb:AI671747 /FEA=EST /DB_XREF=gi:4851478 /DB_XREF=est:wa05e06.x1 /CLONE=IMAGE:2297218 /UG=Hs.81360 Homo sapiens cDNA: FLJ21927 fls, clone HEP04178, highly similar to HSU90909 Human clone 23722 mRNA sequence
219622_at	gb:NM_017817.1 /DEF=Homo sapiens hypothetical protein FLJ20429 (FLJ20429), mRNA. /FEA=mrna /GEN=FLJ20429 /PROD=hypothetical protein FLJ20429 /DB_XREF=gi:8923400 /UG=Hs.179791 hypothetical protein FLJ20429 /FL=gb:NM_017817.1
219190_s_at	gb:NM_017629.1 /DEF=Homo sapiens hypothetical protein FLJ20033 (FLJ20033), mRNA. /FEA=mrna /GEN=FLJ20033 /PROD=hypothetical protein FLJ20033 /DB_XREF=gi:8923033 /UG=Hs.134757 hypothetical protein FLJ20033 /FL=gb:NM_017629.1
208707_at	Consensus includes gb:BE552334 /FEA=EST /DB_XREF=gi:9794026 /DB_XREF=est:hy06c06.x1 /CLONE=IMAGE:3196522 /UG=Hs.286236 eukaryotic translation initiation factor 5 /FL=gb:AL080102.1
218506_x_at	gb:NM_018459.1 /DEF=Homo sapiens uncharacterized bone marrow protein BM045 (BM045), mRNA. /FEA=mrna /GEN=BM045 /PROD=uncharacterized bone marrow protein BM045 /DB_XREF=gi:8922103 /UG=Hs.8750 uncharacterized bone marrow protein BM045 /FL=gb:AF217521.1 gb:NM_018459.1
207545_s_at	gb:NM_003744.1 /DEF=Homo sapiens numb (Drosophila) homolog (NUMB), mRNA. /FEA=mrna /GEN=NUMB /PROD=numb (Drosophila) homolog /DB_XREF=gi:4505478 /UG=Hs.78890 numb (Drosophila) homolog /FL=gb:NM_003744.1 gb:L40393.1

212014_x_at	Consensus includes gb:AI493245 /FEA-EST /DB_XREF=gi:4394248 /DB_XREF=est:t130d08.x1 /CLONE=IMAGE:2131983 /UG=Hs.169610 CD44 antigen (homolog function and Indian blood group system)
209039_x_at	gb:AF001434.1 /DEF=Human HpaI (HPAST) mRNA, complete cds. /FEA=mrna /GEN=HPAST /PROD=HpaI /DB_XREF=gi:2529706 /UG=Hs.155119 EH domain containing 1 /FL=gb:AF001434.1
208650_s_at	Consensus includes gb:BG327863 /FEA-EST /DB_XREF=gi:13134301 /DB_XREF=est:602426876f1 /CLONE=IMAGE:4564675 /UG=Hs.286124 CD24 antigen (small cell lung carcinoma cluster 4 antigen) /FL=gb:IM58664.1 gb:LM33930.1 gb:NM 013230.1
209806_at	gb:BC000893.1 /DEF=Homo sapiens, H2B histone family, member A, clone MGC:5132, mRNA, complete cds. /FEA=mrna /PROD=H2B histone family, member A /DB_XREF=gi:12654150 /UG=Hs.247817 H2B histone family, member A /FL=gb:BC000893.1
212573_at	Consensus includes gb:AF131747.1 /DEF=Homo sapiens clone 24951 mRNA sequence. /FEA=mrna /DB_XREF=gi:4406562 /UG=Hs.167115 KIAA0830 protein
203845_at	Consensus includes gb:AV727449 /FEA-EST /DB_XREF=gi:10836870 /DB_XREF=est:AV727449 /CLONE=HTCAYG01 /UG=Hs.199061 p300CBP-associated factor /FL=gb:U57317.2 gb:NM 003884.2
215806_x_at	Consensus includes gb:MI3231.1 /DEF=Human T-cell receptor aberrantly rearranged gamma-chain mRNA from cell line HEP-MLT. /FEA=mrna /DB_XREF=gi:339168 /UG=Hs.274509 T cell receptor gamma constant 2
202195_s_at	gb:NM 016040.1 /DEF=Homo sapiens CGI-100 protein (LOC503999), mRNA. /FEA=mrna /GEN=LOC503999 /PROD=CGI-100 protein /DB_XREF=gi:7705583 /UG=Hs.296155 CGI-100 protein /FL=gb:AF151858.1 gb:NM 016040.1
201912_s_at	gb:NM 002094.1 /DEF=Homo sapiens G1 to S phase transition 1 (GSPT1), mRNA. /FEA=mrna /GEN=GSPT1 /PROD=G1 to S phase transition 1 /DB_XREF=gi:4504166 /UG=Hs.2707 G1 to S phase transition 1 /FL=gb:NM 002094.1
201712_s_at	gb:NM 006267.2 /DEF=Homo sapiens RAN binding protein 2 (RANBP2), mRNA. /FEA=mrna /GEN=RANBP2 /PROD=RAN binding protein 2 /DB_XREF=gi:6382078 /UG=Hs.199179 RAN binding protein 2 /FL=gb:NM 006267.2 gb:D42063.1
212864_at	Consensus includes gb:Y16521.1 /DEF=Homo sapiens mRNA for CDS2 protein. /FEA=mrna /GEN=CDS2 /PROD=CDS2 protein /DB_XREF=gi:4186022 /UG=Hs.24812 CDP-diacylglycerol synthase (phosphatidate cytidyltransferase) 2
203504_s_at	gb:NM 005502.1 /DEF=Homo sapiens ATP-binding cassette, sub-family A (ABCA1), member 1 (ABCA1), mRNA. /FEA=mrna /GEN=ABCA1 /PROD=ATP-binding cassette, sub-family A member 1 /DB_XREF=gi:5915657 /UG=Hs.211562 ATP-binding cassette, sub-family A (ABCA1), member 1 /FL=gb:AF165281.1 gb:NM 005502.1 gb:AF285167.1
212457_at	Consensus includes gb:AL161985.1 /DEF=Homo sapiens mRNA: cDNA DKFZp761J1810 (from clone DKFZp761J1810). /FEA=mrna /DB_XREF=gi:7328121 /UG=Hs.274184 transcription factor binding to IGHM enhancer 3
214683_s_at	Consensus includes gb:AI251890 /FEA-EST /DB_XREF=gi:3848419 /DB_XREF=est:qu78d12.x1 /CLONE=IMAGE:1978199 /UG=Hs.2083 CDC-like kinase1
44783_s_at	Cluster incl. R61374:ylh5e02.sl Homo sapiens cDNA, 3' end /clone=IMAGE-37665 /clone_end=3 /gb=R61374 /gi=832069 /UG=Hs.234434 /len=434
202252_at	gb:NM 002870.1 /DEF=Homo sapiens RAB13, member RAS oncogene family (RAB13), mRNA. /FEA=mrna /GEN=RAB13 /PROD=RAB13, member RAS oncogene family /DB_XREF=gi:4506362 /UG=Hs.151536 RAB13, member RAS oncogene family /FL=gb:BC000799.1 gb:NM 002870.1
206025_s_at	Consensus includes gb:AW188198 /FEA-EST /DB_XREF=gi:6462634 /DB_XREF=est:xj93f03.x1 /CLONE=IMAGE:2664797 /UG=Hs.29352 tumor necrosis factor, alpha-induced protein 6 /FL=gb:NM 007115.1
203936_s_at	gb:NM 004994.1 /DEF=Homo sapiens matrix metalloproteinase 9 (gelatinase B, 92kD gelatinase, 92kD type IV collagenase) (MMP9), mRNA. /FEA=mrna /GEN=MMP9 /PROD=matrix metalloproteinase 9 (gelatinase B, 92kD gelatinase, 92kD type IV collagenase) /DB_XREF=gi:4826835 /UG=Hs.151738 matrix metalloproteinase 9 (gelatinase B, 92kD gelatinase, 92kD type IV collagenase) /FL=gb:J05070.1 gb:NM 004994.1
221523_s_at	Consensus includes gb:AL138717 /DEF=Human DNA sequence from clone RPL11-11D8 on chromosome 6 Contains the 5' end of the gene for a yeast ubiquitin conjugating enzyme UBC6 homolog, the gene for a possible GTP binding protein, a NACA (nascent-polypeptide-associated complex alpha polypeptide... /FEA=mrna 2 /DB_XREF=gi:8894207 /UG=Hs.238679 Rag D protein /FL=gb:NM 021244.1 gb:AF272036.1 gb:BC003088.1
215785_s_at	Consensus includes gb:AL161999.1 /DEF=Homo sapiens mRNA: cDNA DKFZp761H087 (from clone DKFZp761H087); partial cds. /FEA=mrna /GEN=DKFZp761H087 /PROD=hypothetical protein /DB_XREF=gi:7328000 /UG=Hs.258503 p53 inducible protein
217822_at	gb:NM 016312.1 /DEF=Homo sapiens Npw38-binding protein NpwBP (LOC51729), mRNA. /FEA=mrna /GEN=LOC51729 /PROD=Npw38-binding protein NpwBP /DB_XREF=gi:7706500 /UG=Hs.16420 Npw38-binding protein NpwBP /FL=gb:BC001621.1 gb:AF118023.1 gb:AB029309.1 gb:NM 016312.1
202206_at	Consensus includes gb:AW450363 /FEA-EST /DB_XREF=gi:6991139 /DB_XREF=est:UT-H-B13-akn-d-02-0-UI.s1 /CLONE=IMAGE:2734875 /UG=Hs.111554 ADP-ribosylation factor-like 7 /FL=gb:BC001051.1 gb:AB016811.1 gb:NM 005737.2
202439_s_at	gb:NM 000202.2 /DEF=Homo sapiens iduronate 2-sulfatase (Hunter syndrome) (IDS), transcript variant 1, mRNA. /FEA=mrna /GEN=IDS /PROD=iduronate-2-sulfatase isoform a precursor /DB_XREF=gi:5360215 /UG=Hs.172458 iduronate 2-sulfatase (Hunter syndrome) /FL=gb:IM58342.1 gb:NM 000202.2

213056_at	Consensus includes gb:AUI45019 /FEA=EST /DB_XREF=gi:11006540 /DB_XREF=est:AUI45019 /CLONE=HEMBA1003646 /UG=Hs.96427 KIAA1013 protein
222142_at	Consensus includes gb:AK024212.1 /DEF=Homo sapiens cDNA FLJ14150 fis, clone MAMMA1003026, highly similar to Homo sapiens HSPC057 mRNA. /FEA=mrna /DB_XREF=gi:10436534 /UG=Hs.18827 KIAA0849 protein
214784_x_at	Consensus includes gb:BE966299 /FEA=EST /DB_XREF=gi:1171566 /DB_XREF=est:601660539R1 /CLONE=IMAGE:3906248 /UG=Hs.70500 KIAA0370 protein
222035_s_at	Consensus includes gb:AI984479 /FEA=EST /DB_XREF=gi:5811756 /DB_XREF=est:wr83e06.x1 /CLONE=IMAGE:2494306 /UG=Hs.49007 poly(A) polymerase alpha
212219_at	Consensus includes gb:D38521.1 /DEF=Human mRNA for KIAA0077 gene, partial cds. /FEA=mrna /GEN=KIAA0077 /DB_XREF=gi:559329 /UG=Hs.112396 KIAA0077 protein
214152_at	Consensus includes gb:AUI44243 /FEA=EST /DB_XREF=gi:11005764 /DB_XREF=est:AUI44243 /CLONE=HEMBA1001328 /UG=Hs.247118 phosphatidylinositol glycan, class B
202948_at	gb:NM_000877.1 /DEF=Homo sapiens interleukin 1 receptor, type I (IL1R1), mRNA. /FEA=mrna /GEN=IL1R1 /PROD=interleukin 1 receptor, type I /DB_XREF=gi:4504658 /UG=Hs.82112 interleukin 1 receptor, type I /FL=gb:M27492.1 gb:NM_000877.1
207978_s_at	gb:NM_006981.1 /DEF=Homo sapiens nuclear receptor subfamily 4, group A, member 3 (NR4A3), mRNA. /FEA=mrna /GEN=NR4A3 /PROD=nuclear receptor subfamily 4, group A, member 3 /DB_XREF=gi:11276070 /UG=Hs.80561 nuclear receptor subfamily 4, group A, member 3 /FL=gb:NM_006981.1 gb:D78579.1
209304_x_at	gb:AF087853.1 /DEF=Homo sapiens growth arrest and DNA damage inducible protein beta (GADD45B) mRNA, complete cds. /FEA=mrna /GEN=GADD45B /PROD=growth arrest and DNA damage inducible protein beta /DB_XREF=gi:12061050 /UG=Hs.110571 growth arrest and DNA-damage-inducible, beta /FL=gb:AF087853.1 gb:AF078077.1
214783_s_at	Consensus includes gb:BG177920 /FEA=EST /DB_XREF=gi:12684623 /DB_XREF=est:602327839F1 /CLONE=IMAGE:4429256 /UG=Hs.75510 annexin A11
46270_at	Cluster Incl. AL039447:DKFZp434N1010_s1 Homo sapiens CDNA, 3' end /clone=DKFZp434N1010 /clone_end=3 /gb=AL039447 /gi=5408497 /ug=Hs.75425 /len=841
221760_at	Consensus includes gb:BG287153 /FEA=EST /DB_XREF=gi:13040709 /DB_XREF=est:602381868F1 /CLONE=IMAGE:4499393 /UG=Hs.25253 mannosidase, alpha, class IA, member 1
210118_s_at	gb:M15329.1 /DEF=Human interleukin 1-alpha (IL1A) mRNA, complete cds. /FEA=mrna /GEN=IL1A /PROD=interleukin 1-alpha /DB_XREF=gi:186277 /UG=Hs.1722 interleukin 1, alpha /FL=gb:M15329.1
204781_s_at	gb:NM_000043.1 /DEF=Homo sapiens tumor necrosis factor receptor superfamily, member 6 (TNFRSF6), mRNA. /FEA=mrna /GEN=TNFRSF6 /PROD=apoptosis (APO-1) antigen 1 /DB_XREF=gi:4507582 /UG=Hs.82359 tumor necrosis factor receptor superfamily, member 6 /FL=gb:M67454.1 gb:NM_000043.1
207677_s_at	gb:NM_013416.1 /DEF=Homo sapiens neutrophil cytosolic factor 4 (NCF4), transcript variant 2, mRNA. /FEA=mrna /GEN=NCF4 /PROD=neutrophil cytosolic factor 4 (40kD), isoform 2 /DB_XREF=gi:7382492 /UG=Hs.196352 neutrophil cytosolic factor 4 (40kD) /FL=gb:BC002798.1 gb:AB025219.1 gb:NM_013416.1
206302_s_at	gb:NM_019094.1 /DEF=Homo sapiens nudix (nucleoside diphosphate linked moiety X)-type motif 4 (NUDT4), mRNA. /FEA=mrna /GEN=NUDT4 /PROD=nudix (nucleoside diphosphate linked moiety X)-type motif 4 /DB_XREF=gi:10800135 /UG=Hs.92381
219460_s_at	nudix (nucleoside diphosphate linked moiety X)-type motif 4 /FL=gb:NM_019094.1 gb:AF191649.1 gb:AF191650.1 gb:AF191653.1
219460_s_at	gb:NM_017849.1 /DEF=Homo sapiens hypothetical protein FLJ20507 (FLJ20507), mRNA. /FEA=mrna /GEN=FLJ20507 /PROD=hypothetical protein FLJ20507 /DB_XREF=gi:8923465 /UG=Hs.202955 hypothetical protein FLJ20507 /FL=gb:NM_017849.1
212225_at	Consensus includes gb:AL516854 /FEA=EST /DB_XREF=gi:12780347 /DB_XREF=est:AL516854 /CLONE=CSDDA007YB20 (5 prime) /UG=Hs.150580 putative translation initiation factor
204479_at	gb:NM_012383.1 /DEF=Homo sapiens osteoclast stimulating factor 1 (OSTF1), mRNA. /FEA=mrna /GEN=OSTF1 /PROD=osteoclast stimulating factor 1 /DB_XREF=gi:6912563 /UG=Hs.95821 osteoclast stimulating factor 1 /FL=gb:U63717.1 gb:NM_012383.1
216457_s_at	Consensus includes gb:AK026080.1 /DEF=Homo sapiens cDNA: FLJ22427 fis, clone HRC09013. /DB_XREF=gi:10438814 /UG=Hs.288883 splicing factor 3a, subunit 1, 120kD
212676_at	Consensus includes gb:AW293356 /FEA=EST /DB_XREF=gi:6699992 /DB_XREF=est:UT-H-BI2-ahl-c-11-0-UT.s1 /CLONE=IMAGE:2727165 /UG=Hs.58220 Homo sapiens cDNA: FLJ23005 fis, clone LING00396, highly similar to AF055023 Homo sapiens clone 24723 mRNA sequence
203675_at	gb:NM_005013.1 /DEF=Homo sapiens nucleobindin 2 (NUCB2), mRNA. /FEA=mrna /GEN=NUCB2 /PROD=nucleobindin 2 /DB_XREF=gi:4826869 /UG=Hs.3164 nucleobindin 2 /FL=gb:AF052643.1 gb:AF052644.1 gb:NM_005013.1
221156_x_at	gb:NM_004748.1 /DEF=Homo sapiens cell cycle progression 8 protein (CPR8), mRNA. /FEA=mrna /GEN=CPR8 /PROD=cell cycle progression 8 protein /DB_XREF=gi:4758047 /UG=Hs.283753 cell cycle progression 8 protein /FL=gb:AF011794.1 gb:NM_004748.1
207791_s_at	gb:NM_004161.1 /DEF=Homo sapiens RAB1, member RAS oncogene family (RAB1), mRNA. /FEA=mrna /GEN=RAB1 /PROD=RAB1,

	member RAS oncogene family /DB_XREF=gi:4758987 /UG=Hs.3642 RAB1, member RAS oncogene family /FL=gb:NM_004161.1 gb:M28209.1
200692_s_at	gb:NM_004134.1 /DEF=Homo sapiens heat shock 70KD protein 9B (mortalin-2) (HSPA9B), mRNA. /FEA=mRNA /GEN=HSPA9B /PROD=heat shock 70KD protein 9B (mortalin-2) /DB_XREF=gi:4758569 /UG=Hs.3069 heat shock 70KD protein 9B (mortalin-2) /FL=gb:BC000478.1 gb:LJ15189.1 gb:NM_004134.1
218936_s_at	gb:NM_014167.1 /DEF=Homo sapiens HSPC128 protein (HSPC128), mRNA. /FEA=mRNA /GEN=HSPC128 /PROD=HSPC128 protein /DB_XREF=gi:7661789 /UG=Hs.90527 HSPC128 protein /FL=gb:AF213377.1 gb:AF161477.1 gb:NM_014167.1
213931_at	Consensus includes gb:AJ1819238 /FEA=EST /DB_XREF=gi:5438328 /DB_XREF=est:wj42q05.xl /CLONE=IMAGE:2405528 /UG=Hs.180919 inhibitor of DNA binding 2, dominant negative helix-loop-helix protein
218247_s_at	gb:NM_016626.1 /DEF=Homo sapiens hypothetical protein (LOC51320), mRNA. /FEA=mRNA /GEN=LOC51320 /PROD=hypothetical protein /DB_XREF=gi:7706165 /UG=Hs.12830 hypothetical protein /FL=gb:AF208855.1 gb:NM_016626.1
213935_at	Consensus includes gb:AF007132.1 /DEF=Homo sapiens clone 23551 mRNA sequence. /FEA=mRNA /DB_XREF=gi:2852606 /UG=Hs.184019 Homo sapiens clone 23551 mRNA sequence
208815_x_at	gb:AB023420.1 /DEF=Homo sapiens mRNA for heat shock protein apg-2, complete cds. /FEA=mRNA /GEN=apg-2 /PROD=apg-2 /DB_XREF=gi:4579908 /UG=Hs.90093 heat shock 70KD protein 4 /FL=gb:AB023420.1
218177_at	Consensus includes gb:AA293502 /FEA=EST /DB_XREF=gi:1941036 /DB_XREF=est:zt53h06.r1 /CLONE=IMAGE:726107 /UG=Hs.42733 CRMP1.5 protein /FL=gb:AF281064.1 gb:NM_020412.1
200648_s_at	gb:NM_002065.1 /DEF=Homo sapiens glutamate-ammonia ligase (glutamine synthase) (GLUL), mRNA. /FEA=mRNA /GEN=GLUL /PROD=glutamate-ammonia ligase (glutamine synthase) /DB_XREF=gi:4504026 /UG=Hs.170171
202843_at	gb:NM_012328.1 /DEF=Homo sapiens microvascular endothelial differentiation gene 1 (MDG1), mRNA. /FEA=mRNA /GEN=MDG1 /PROD=microvascular endothelial differentiation gene 1 (MDG1) /DB_XREF=gi:9558754 /UG=Hs.6790 DnaJ (Hsp40) homolog, subfamily B, member 9 /FL=gb:AF083247.1 gb:AL080081.1 gb:AB026908.1 gb:NM_012328.1
214578_s_at	Consensus includes gb:AV683882 /FEA=EST /DB_XREF=gi:10285745 /DB_XREF=est:AV683882 /CLONE=GKCAIC05 /UG=Hs.17820 Rho-associated, coiled-coil containing protein kinase 1 /FL=gb:U43195.1 gb:NM_005406.1
217473_x_at	Consensus includes gb:AF229163 /DEF=Homo sapiens natural resistance-associated macrophage protein 1 (SLC11A1) gene, complete cds, alternatively spliced; and nuclear LIM interactor-interacting factor (NLI-IF) gene, complete cds /FEA=mRNA_3 /DB_XREF=gi:10257408 /UG=Hs.182611 solute carrier family 11 (proton-coupled divalent metal ion transporters), member 1
207624_s_at	gb:NM_000328.1 /DEF=Homo sapiens retinitis pigmentosa GTPase regulator (RPGR), mRNA. /FEA=mRNA /GEN=RPGR /PROD=retinitis pigmentosa GTPase regulator /DB_XREF=gi:4506580 /UG=Hs.153614 retinitis pigmentosa GTPase regulator /FL=gb:U57629.1 gb:NM_000328.1
202778_s_at	gb:NM_003453.1 /DEF=Homo sapiens zinc finger protein 198 (ZNF198), mRNA. /FEA=mRNA /GEN=ZNF198 /PROD=zinc finger protein 198 /DB_XREF=gi:4508010 /UG=Hs.109526 zinc finger protein 198 /FL=gb:AF035374.1 gb:AF060181.1 gb:NM_003453.1
200653_s_at	gb:M27319.1 /DEF=Human calmodulin mRNA, complete cds. /FEA=mRNA /PROD=calmodulin /DB_XREF=gi:179809 /UG=Hs.177656 calmodulin 1 (phosphorylase kinase, delta) /FL=gb:M27319.1 gb:NM_006888.1
218627_at	gb:NM_018370.1 /DEF=Homo sapiens hypothetical protein FLJ11259 (FLJ11259), mRNA. /FEA=mRNA /GEN=FLJ11259 /PROD=hypothetical protein FLJ11259 /DB_XREF=gi:8922957 /UG=Hs.18465 hypothetical protein FLJ11259 /FL=gb:NM_018370.1
202059_s_at	gb:NM_002264.1 /DEF=Homo sapiens karyopherin alpha 1 (importin alpha 5) (KPNAL1), mRNA. /FEA=mRNA /GEN=KPNAL1 /PROD=karyopherin alpha 1 /DB_XREF=gi:4504894 /UG=Hs.169149 karyopherin alpha 1 (importin alpha 5) /FL=gb:BC002374.1
218132_s_at	gb:BC003009.1 gb:NM_002264.1
218132_s_at	gb:NM_024075.1 /DEF=Homo sapiens LENG5 protein (LENG5), mRNA. /FEA=mRNA /GEN=LENG5 /PROD=LENG5 protein /DB_XREF=gi:13129061 /UG=Hs.15580 LENG5 protein /FL=gb:BC000944.2 gb:NM_024075.1
203265_s_at	Consensus includes gb:AA810268 /FEA=EST /DB_XREF=gi:2879627 /DB_XREF=est:odl4f07.s1 /CLONE=IMAGE:1367941 /UG=Hs.75217 mitogen-activated protein kinase kinase 4 /FL=gb:NM_003010.1 gb:L36870.1 gb:U17743.1
209694_at	gb:M97655.1 /DEF=Human 6-pyruvoyltetrahydropterin synthase (PTS) mRNA, complete cds. /FEA=mRNA /GEN=PTS /PROD=6-pyruvoyltetrahydropterin synthase /DB_XREF=gi:306438 /UG=Hs.366 6-pyruvoyltetrahydropterin synthase /FL=gb:M97655.1 gb:NM_000317.1 gb:DL17400.1
217591_at	Consensus includes gb:BF725121 /FEA=EST /DB_XREF=gi:12041032 /DB_XREF=est:bx12e01.xl /CLONE=bx12e01 /UG=Hs.272108 ESTs
222309_at	Consensus includes gb:AW972292 /FEA=EST /DB_XREF=gi:8162138 /DB_XREF=est:EST384381 /UG=Hs.292998 ESTs

201627_s_at	gb:NM_005542.1 /DEF=Homo sapiens insulin induced gene 1 (INSIG1), mRNA. /FEA=mrna /GEN=INSIG1 /PROD=insulin induced gene 1 /DB_XREF=gi:5031800 /UG=Hs.56205 insulin induced gene 1 /FL=gb:NM_005542.1
217249_x_at	Consensus includes gb:AC004544 /DEF=Homo sapiens BAC clone CTB-162B4 from 4 /FEA=CDS /DB_XREF=gi:3041843 /UG=Hs.248095 Homo sapiens BAC clone CTB-162B4 from 4
220496_at	gb:NM_016509.1 /DEF=Homo sapiens C-type lectin-like receptor-2 (LOC51266), mRNA. /FEA=mrna /GEN=LOC51266 /PROD=C-type lectin-like receptor-2 /DB_XREF=gi:114231 C-type lectin-like receptor-2 /FL=gb:AF124841.1 gb:NM_016509.1
201096_s_at	Consensus includes gb:AL537042 /FEA=EST /DB_XREF=gi:12800535 /DB_XREF=est:AL537042 /CLONE=CS0DF017YF17 (5 prime) /UG=Hs.75290 ADP-ribosylation factor 4 /FL=gb:BC003364.1 gb:NM_001660.2
201580_s_at	Consensus includes gb:AL544094 /FEA=EST /DB_XREF=gi:12876573 /DB_XREF=est:AL544094 /CLONE=CS0DI004YG20 (3 prime) /UG=Hs.169358 hypothetical protein /FL=gb:NM_021156.1
201109_s_at	Consensus includes gb:AV726673 /FEA=EST /DB_XREF=gi:10836094 /DB_XREF=est:AV726673 /CLONE=HTCBGC12 /UG=Hs.87409 thrombospondin 1 /FL=gb:NM_003246.1
203080_s_at	gb:NM_013450.1 /DEF=Homo sapiens bromodomain adjacent to zinc finger domain, 2B (BAZ2B), mRNA. /FEA=mrna /GEN=BAZ2B /PROD=bromodomain adjacent to zinc finger domain, 2B /DB_XREF=gi:7304922 /UG=Hs.8383 bromodomain adjacent to zinc finger domain, 2B /FL=gb:AB032255.1 gb:NM_013450.1
202558_s_at	gb:NM_006948.1 /DEF=Homo sapiens stress 70 protein chaperone, microsome-associated, 60kD (STCH), mRNA. /FEA=mrna /GEN=STCH /PROD=stress 70 protein chaperone, microsome-associated, 60kD /DB_XREF=gi:5902125 /UG=Hs.288799 stress 70 protein chaperone, microsome-associated, 60kD /FL=gb:U04735.1 gb:NM_006948.1
201349_at	gb:NM_004252.1 /DEF=Homo sapiens solute carrier family 9 (sodium/hydrogen exchanger), isoform 3 regulatory factor 1 (SLC9A3R1), mRNA. /FEA=mrna /GEN=SLC9A3R1 /PROD=solute carrier family 9 (sodium/hydrogen exchanger), isoform 3 regulatory factor 1 /DB_XREF=gi:4759139 /UG=Hs.184276 solute carrier family 9 (sodium/hydrogen exchanger), isoform 3 regulatory factor 1 /FL=gb:BC001443.1 gb:BC003361.1 gb:AF036241.1 gb:AF015926.1 gb:NM_004252.1
220603_s_at	gb:NM_018349.1 /DEF=Homo sapiens hypothetical protein FLJ11175 (FLJ11175), mRNA. /FEA=mrna /GEN=FLJ11175 /PROD=hypothetical protein FLJ11175 /DB_XREF=gi:8922916 /UG=Hs.33368 hypothetical protein FLJ11175 /FL=gb:NM_018349.1
35820_at	Cluster Incl. X62078:H.sapiens mRNA for GM2 activator protein /cds=UNKNOWN /gb=X62078 /gi=313158 /ug=Hs.69743 /len=2436
201731_s_at	gb:NM_003292.1 /DEF=Homo sapiens translocated promoter region (to activated MET oncogene) (TPR), mRNA. /FEA=mrna /GEN=TPR /PROD=translocated promoter region (to activated MET oncogene) /DB_XREF=gi:4507658 /UG=Hs.169750 translocated promoter region (to activated MET oncogene) /FL=gb:NM_003292.1
202414_at	gb:NM_000123.1 /DEF=Homo sapiens excision repair cross-complementing rodent repair deficiency, complementation group 5 (xeroderma pigmentosum, complementation group G (Cockayne syndrome)) (ERCC5), mRNA. /FEA=mrna /GEN=ERCC5 /PROD=xpg-complementing protein /DB_XREF=gi:4503600 /UG=Hs.48576 excision repair cross-complementing rodent repair deficiency, complementation group 5 (xeroderma pigmentosum, complementation group G (Cockayne syndrome)) /FL=gb:U16305.1 gb:L20046.1 gb:NM_000123.1
210422_x_at	gb:D50402.1 /DEF=Human mRNA for NRAMP1, complete cds. /FEA=mrna /PROD=Nramp /DB_XREF=gi:1000996 /UG=Hs.182611 solute carrier family 11 (proton-coupled divalent metal ion transporters), member 1 /FL=gb:D50402.1 gb:D50403.1 gb:NM_000578.1 gb:L32185.1
58900_at	Cluster Incl. AW025284:wu95h10.x1 Homo sapiens cDNA, 3' end /clone=IMAGE-990806 /clone_end=3 /gb=AW025284 /gi=5878814 /ug=Hs.237946 /len=454
219890_at	gb:NM_013252.1 /DEF=Homo sapiens C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 5 (CLC5F5), mRNA. /FEA=mrna /GEN=CLC5F5 /PROD=C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 5 /DB_XREF=gi:10281668 /UG=Hs.126355 C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 5 /FL=gb:NM_013252.1 gb:AF139768.1
208112_x_at	gb:NM_006795.1 /DEF=Homo sapiens EH domain containing 1 (EHD1), mRNA. /FEA=mrna /GEN=EHD1 /PROD=EH domain containing 1 /DB_XREF=gi:5803008 /UG=Hs.155119 EH domain containing 1 /FL=gb:AF099011.1 gb:NM_006795.1
218655_s_at	gb:NM_017748.1 /DEF=Homo sapiens hypothetical protein FLJ20291 (FLJ20291), mRNA. /FEA=mrna /GEN=FLJ20291 /PROD=hypothetical protein FLJ20291 /DB_XREF=gi:8923270 /UG=Hs.8928 hypothetical protein FLJ20291 /FL=gb:NM_017748.1
214230_at	Consensus includes gb:R37664 /FEA=EST /DB_XREF=gi:795120 /DB_XREF=est:yf61e05.s1 /CLONE=IMAGE:26577 /UG=Hs.146409 cell division cycle 42 (GTP-binding protein, 25kD)
201898_s_at	Consensus includes gb:AL126625 /FEA=EST /DB_XREF=gi:3595139 /DB_XREF=est:qd83a12.x1 /CLONE=IMAGE:1736062 /UG=Hs.80612 ubiquitin-conjugating enzyme E2A (RAD6 homolog) /FL=gb:M74524.1 gb:NM_003336.1

210773_s_at	gb:U81501.1 /DEF=Human lipoxin A4 receptor mRNA, complete cds. /FEA=mRNA /PROD=lipoxin A4 receptor /DB_XREF=gi:1916075 /UG=Hs.99855 formyl peptide receptor-like 1 /FL=gb:M76672.1 gb:M84562.1 gb:M88107.1 gb:U81501.1 gb:AF054013.1
32069_at	gb:NM_001462.1
Cluster Incl.	AB014515: Homo sapiens mRNA for KIAA0615 protein, complete cds /cds=(237,2927) /gb=AB014515 /gi=3327043 /ug=Hs.155972 /len=3319
121_at	X69699 /FEATURE= /DEFINITION=HSPAX3A H.sapiens Pax8 mRNA
202053_s_at	gb:L47162.1 /DEF=Human fatty aldehyde dehydrogenase (FALDH) mRNA, complete cds. /FEA=mRNA /GEN=FALDH /PROD=fatty aldehyde dehydrogenase /DB_XREF=gi:1082035 /UG=Hs.159608 aldehyde dehydrogenase 3 family, member A2 /FL=gb:L47162.1
212335_at	gb:U46689.1 gb:NM_000382.1
209813_x_at	Consensus includes gb:AW167793 /FEA=EST /DB_XREF=gi:6399401 /DB_XREF=est:yg56d07.x1 /CLONE=IMAGE:2632333 /UG=Hs.164036
204747_at	gb:NM_001549.1 /DEF=Homo sapiens T-cell receptor gamma chain VUC1-CII region mRNA, complete cds. /FEA=mRNA /GEN=TCRG /DB_XREF=gi:339399 /UG=Hs.112259 T cell receptor gamma locus /FL=gb:M16768.1 gb:AF151103.1
204747_at	gb:NM_001549.1 /DEF=Homo sapiens interferon-induced protein with tetratricopeptide repeats 4 (IFIT4), mRNA. /FEA=mRNA /GEN=IFIT4 /PROD=interferon-induced protein with tetratricopeptide repeats 4 /DB_XREF=gi:4504586 /UG=Hs.181874
212223_at	Interferon-induced protein with tetratricopeptide repeats 4 /FL=gb:BC001383.1 gb:BC004977.1 gb:U52513.1 gb:AF026939.1
218880_at	gb:AF083470.1 gb:NM_001549.1
202460_s_at	Consensus includes gb:AI926544 /FEA=EST /DB_XREF=gi:5662508 /DB_XREF=est:wo46cl2.x1 /CLONE=IMAGE:2458390 /UG=Hs.303154
58780_s_at	Consensus includes gb:N36408 /FEA=EST /DB_XREF=gi:1157550 /DB_XREF=est:YV33F03.s1 /CLONE=IMAGE:273053 /UG=Hs.325364
205281_s_at	hypothetical protein FLJ23306 /FL=gb:NM_024530.1
218251_at	gb:NM_014646.1 /DEF=Homo sapiens lipin 2 (LPIN2), mRNA. /FEA=mRNA /GEN=LPIN2 /PROD=lipin 2 /DB_XREF=gi:7662021 /UG=Hs.166318 lipin 2 /FL=gb:D87436.1 gb:NM_014646.1
212481_s_at	Cluster Incl. R42449:yg02a07.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-30831 /clone_end=3 /gb=R42449 /gi=817213 /ug=Hs.235831 /len=431
212481_s_at	gb:NM_002641.1 /DEF=Homo sapiens phosphatidylinositol glycan, class A (paroxysmal nocturnal hemoglobinuria) (PIGA), transcript variant 1, mRNA. /FEA=mRNA /GEN=PIGA /PROD=phosphatidylinositol glycan, class A isoform 1 /DB_XREF=gi:11863129 /UG=Hs.51 phosphatidylinositol glycan, class A (paroxysmal nocturnal hemoglobinuria) /FL=gb:NM_002641.1 gb:D11466.1
212481_s_at	gb:NM_021242.1 /DEF=Homo sapiens hypothetical protein STRAIT11499 (STRAIT11499), mRNA. /FEA=mRNA /GEN=STRAIT11499 /PROD=hypothetical protein STRAIT11499 /DB_XREF=gi:10864050 /UG=Hs.236556 hypothetical protein STRAIT11499 /FL=gb:NM_021242.1
212481_s_at	Consensus includes gb:AI214061 /FEA=EST /DB_XREF=gi:3777662 /DB_XREF=est:ap29d10.x1 /CLONE=IMAGE:1956787 /UG=Hs.250641 tropomyosin 4
213292_s_at	Consensus includes gb:AA908770 /FEA=EST /DB_XREF=gi:3048175 /DB_XREF=est:o106a11.s1 /CLONE=IMAGE:1522652 /UG=Hs.283881 KIAA0713 protein
221497_x_at	gb:BC005369.1 /DEF=Homo sapiens, chromosome 1 open reading frame 12, clone MGC:12484, mRNA, complete cds. /FEA=mRNA /PROD=chromosome 1 open reading frame 12 /DB_XREF=gi:13529208 /UG=Hs.6523 chromosome 1 open reading frame 12 /FL=gb:AF229245.1 gb:AF27176.1 gb:NM_022051.1 gb:BC005369.1
212185_x_at	Consensus includes gb:NM_005953.1 /DEF=Homo sapiens metallothionein 2A (MT2A), mRNA. /FEA=CDS /GEN=MT2A /PROD=metalothionein 2A /DB_XREF=gi:5174763 /UG=Hs.118786 metallothionein 2A /FL=gb:NM_005953.1
203961_at	Consensus includes gb:AL157398 /DEF=Human DNA sequence from clone RPL1-56H7 on chromosome 10. Contains ESTs, STSs and GSSs. Contains the gene for the nebulin protein (NEBL, actin-binding Z-disc protein) /FEA=mRNA_1 /DB_XREF=gi:10045326 /UG=Hs.5025 nebulin /FL=gb:NM_006393.1
210986_s_at	gb:Z24727.1 /DEF=H.sapiens tropomyosin isoform mRNA, complete cds. /FEA=mRNA /PROD=tropomyosin isoform /DB_XREF=gi:854188 /UG=Hs.77899 tropomyosin 1 (alpha) /FL=gb:Z24727.1
41386_i_at	Cluster Incl. AB002344: Human mRNA for KIAA0346 gene, partial cds /cds=(0,4852) /gb=AB002344 /gi=2280479 /ug=Hs.103915 /len=6121
201874_at	Consensus includes gb:BF978611 /FEA=EST /DB_XREF=gi:12345826 /DB_XREF=est:602149061f1 /CLONE=IMAGE:4307822 /UG=Hs.14891 hypothetical protein FLJ21047 /FL=gb:NM_024569.1
211781_x_at	gb:BC006164.1 /DEF=Homo sapiens, clone MGC:13219, mRNA, complete cds. /FEA=mRNA /PROD=Unknown (protein for MGC:13219) /DB_XREF=gi:13544062 /FL=gb:BC006164.1
202459_s_at	Consensus includes gb:U55968 /FEA=EST /DB_XREF=gi:1354524 /DB_XREF=est:HSU55968 /CLONE=26508 /UG=Hs.166318 lipin 2 /FL=gb:D87436.1 gb:NM_014646.1

217908_s_at	gb:NM 018442.1 /DEF=Homo sapiens PC326 protein (PC326), mRNA. /FEA=mRNA /GEN=PC326 /PROD=PC326 protein /DB_XREF=gi:8923955 /UG=Hs.279882 PC326 protein /FL=gb:AL336738.1 gb:AF150734.1 gb:NM 018442.1
202427_s_at	gb:NM 015415.1 /DEF=Homo sapiens DKFZP564B167 protein (DKFZP564B167), mRNA. /FEA=mRNA /GEN=DKFZP564B167 /PROD=DKFZP564B167 protein /DB_XREF=gi:7661601 /UG=Hs.76285 DKFZP564B167 protein /FL=gb:AL110297.1 gb:NM 015415.1
213716_s_at	Consensus includes gb:BF939675 /FEA=EST /DB_XREF=est:nac79g07.x1 /CLONE=IMAGE:3440820 /UG=Hs.326612
212550_at	Homo sapiens secreted and transmembrane 1 (SECTM1), mRNA
33323_r_at	Consensus includes gb:AL149535 /FEA=EST /DB_XREF=gi:3678004 /DB_XREF=est:cq70f11.x1 /CLONE=IMAGE:1714989 /UG=Hs.24064 Homo sapiens mRNA; cDNA DKFZP586N1323 (from clone DKFZP586N1323)
220947_s_at	Cluster Incl. X57348:H.sapiens mRNA (clone 9112) /cds=(165,911) /gb=X57348 /gi=23939 /ug=Hs.184510 /len=1407
202665_s_at	gb:NM 015527.1 /DEF=Homo sapiens DKFZP434P1750 protein (DKFZP434P1750), mRNA. /FEA=mRNA /GEN=DKFZP434P1750 /PROD=DKFZP434P1750 protein /DB_XREF=gi:7661587 /UG=Hs.7274 DKFZP434P1750 protein /FL=gb:NM 015527.1
220746_s_at	gb:NM 003387.2 /DEF=Homo sapiens Wiskott-Aldrich syndrome protein interacting protein (WASP-IP), mRNA. /FEA=mRNA /GEN=WASP-IP /PROD=WASP-IP-interacting protein /DB_XREF=gi:8400739 /UG=Hs.24143 Wiskott-Aldrich syndrome protein interacting protein /FL=gb:NM 003387.2
218078_s_at	gb:NM 016290.1 /DEF=Homo sapiens retinoid x receptor interacting protein (LOC51720), mRNA. /FEA=mRNA /GEN=LOC51720 /PROD=retinoid x receptor interacting protein /DB_XREF=gi:7706482 /UG=Hs.7889 retinoid x receptor interacting protein /FL=gb:AF113538.1 gb:NM 016290.1
203429_s_at	gb:NM 016598.1 /DEF=Homo sapiens DHHC1 protein (LOC51304), mRNA. /FEA=mRNA /GEN=LOC51304 /PROD=DHHC1 protein /DB_XREF=gi:7706132 /UG=Hs.14896 DHHC1 protein /FL=gb:AF247703.1 gb:NM 016598.1
203120_at	gb:NM 016227.1 /DEF=Homo sapiens membrane protein CH1 (CH1), mRNA. /FEA=mRNA /GEN=CH1 /PROD=membrane protein CH1 /DB_XREF=gi:7705321 /UG=Hs.108636 membrane protein CH1 /FL=gb:AF097535.1 gb:NM 016227.1
203143_s_at	gb:NM 005426.1 /DEF=Homo sapiens tumor protein p53-binding protein, 2 (TP53BP2), mRNA. /FEA=mRNA /GEN=TP53BP2 /PROD=tumor protein p53-binding protein, 2 /DB_XREF=gi:4885642 /UG=Hs.44585 tumor protein p53-binding protein, 2 /FL=gb:U58334.1 gb:NM 005426.1
41387_r_at	Consensus includes gb:T79953 /FEA=EST /DB_XREF=gi:598462 /DB_XREF=est:y085c11.s1 /CLONE=IMAGE:115028 /UG=Hs.158282 KIAA0040 gene product /FL=gb:D25539.1 gb:NM 014656.1
202286_s_at	Cluster Incl. AB002344:Human mRNA for KIAA0346 gene, partial cds /cds=(0,4852) /gb=AB002344 /gi=2280479 /ug=Hs.103915 /len=6121
200670_at	Consensus includes gb:J04152 /DEF=Human gastrointestinal tumor-associated antigen GA733-1 protein gene, complete cds, clone 05516 /FEA=mRNA /DB_XREF=gi:182893 /UG=Hs.23582 tumor-associated calcium signal transducer 2 /FL=gb:NM 002353.1
211612_s_at	gb:NM 005080.1 /DEF=Homo sapiens X-box binding protein 1 (XBPL), mRNA. /FEA=mRNA /GEN=XBPL /PROD=X-box binding protein 1 /DB_XREF=gi:4827057 /UG=Hs.149923 X-box binding protein 1 /FL=gb:BC000938.1 gb:NM 005080.1
203233_at	gb:U62858.1 /DEF=Human interleukin-13 receptor mRNA, complete cds. /FEA=mRNA /PROD=interleukin-13 receptor /DB_XREF=gi:1695875 /FL=gb:U62858.1
204507_s_at	gb:NM 000418.1 /DEF=Homo sapiens interleukin 4 receptor (IL4R), mRNA. /FEA=mRNA /GEN=IL4R /PROD=interleukin 4 receptor precursor /DB_XREF=gi:4557668 /UG=Hs.75545 interleukin 4 receptor /FL=gb:NM 000418.1
218136_s_at	gb:NM 000945.1 /DEF=Homo sapiens protein phosphatase 3 (formerly 2B), regulatory subunit B (19kD), alpha isoform (calcineurin B, type I) (PPP3R1), mRNA. /FEA=mRNA /GEN=PPP3R1 /PROD=protein phosphatase 3 (formerly 2B), regulatory subunit B (19kD), alpha isoform (calcineurin B, type I) /DB_XREF=gi:4506024 /UG=Hs.278540 protein phosphatase 3 (formerly 2B), regulatory subunit B (19kD), alpha isoform (calcineurin B, type I) /FL=gb:M30773.1 gb:NM 000945.1
201582_at	gb:NM 018579.1 /DEF=Homo sapiens mitochondrial solute carrier (LOC51312), mRNA. /FEA=mRNA /GEN=LOC51312 /PROD=hypothetical protein PRO1278 /DB_XREF=gi:8924027 /UG=Hs.300496 mitochondrial solute carrier /FL=gb:AF153660.1 gb:AF116630.1 gb:NM 018579.1
209339_at	Consensus includes gb:AL121900 /DEF=Human DNA sequence from clone RFL1-37935 on chromosome 20 Contains the last exon of the SEC23B gene for Sec23 (S. cerevisiae) homolog B, a putative novel gene, the 5' end of the gene for a novel protein similar to bacterial histidyl-tRNA synthetase... /FEA=mRNA /DB_XREF=gi:11121203 /UG=Hs.173497 Sec23 (S. cerevisiae) homolog B /FL=gb:BC005404.1 gb:NM 006363.1
208030_s_at	gb:U76248.1 /DEF=Human H2AH2 mRNA, complete cds. /FEA=mRNA /PROD=H2AH2 /DB_XREF=gi:2673967 /UG=Hs.20191 seven in absentia (Drosophila) homolog 2 /FL=gb:U76248.1 gb:NM 005067.1
	gb:NM 001119.2 /DEF=Homo sapiens adducin 1 (alpha) (ADD1), transcript variant 1, mRNA. /FEA=mRNA /GEN=ADD1 /PROD=adducin 1 (alpha) isoform a /DB_XREF=gi:7710113 /FL=gb:NM 001119.2

201195_s_at	gb:AB018009.1 /DEF=Homo sapiens mRNA for L-type amino acid transporter 1, complete cds. /FEA=mRNA /GEN=hLAT1 /PROD=L-type amino acid transporter 1 /DB XREF=gi:5926731 /UG=Hs.184601 solute carrier family 7 (cationic amino acid transporter, y+ system), member 5 /FL=gb:AF077866.1 gb:AB018542.1 gb:AF104032.1 gb:NM_003486.1 gb:AB017908.1 gb:AB018009.1
217918_at	gb:NM_014183.1 /DEF=Homo sapiens HSPC162 protein (HSPC162), mRNA. /FEA=mRNA /GEN=HSPC162 /PROD=HSPC162 protein /DB XREF=gi:7661821 /UG=Hs.100002 HSPC162 protein /FL=gb:BC002481.1 gb:AY026513.1 gb:AF161511.1 gb:NM_014183.1 gb:AF165516.1

Tabelle 4: Gene aus Clusteranalyse 4

Affymetrix interne Bezeichnung	Beschreibung der Sequenz in der Genebank Datenbank
221798_x_at	Consensus includes gb:AI183766 /FEA=EST /DB_XREF=gi:3734404 /DB_XREF=est:qel7g06.x1 /CLONE=IMAGE:1739290 /UG=Hs.182426 ribosomal protein S2
218231_at	gb:NM_017567.1 /DEF=Homo sapiens N-Acetylglucosamine kinase (HSA242910), mRNA. /FEA=mrna /GEN=HSA242910 /PROD=N-Acetylglucosamine kinase /DB_XREF=gi:8923736 /UG=Hs.7036 N-Acetylglucosamine kinase /FL=gb:BC001029.1 gb:NM_017567.1
201009_s_at	Consensus includes gb:AI439556 /FEA=EST /DB_XREF=gi:4305149 /DB_XREF=est:tc90c12.x1 /CLONE=IMAGE:2073430 /UG=Hs.179526 upregulated by 1,25-dihydroxyvitamin D-3 /FL=gb:NM_006472.1 gb:S73591.1
212998_x_at	Consensus includes gb:AI583173 /FEA=EST /DB_XREF=gi:4569070 /DB_XREF=est:tq64e04.x1 /CLONE=IMAGE:2213598 /UG=Hs.73931 major histocompatibility complex, class II, DQ beta 1
201464_x_at	Consensus includes gb:BG491844 /FEA=EST /DB_XREF=gi:13453356 /DB_XREF=est:602535931T1 /CLONE=IMAGE:4684998 /UG=Hs.78465 v-jun avian sarcoma virus 17 oncogene homolog /FL=gb:BC002646.1 gb:NM_002228.2
214687_x_at	Consensus includes gb:AK026577.1 /DEF=Homo sapiens cDNA: FLJ22924 fis, clone KAT06977, highly similar to HSA1DAR Human fibroblast mRNA for aldolase A. /FEA=mrna /DB_XREF=gi:10439461 /UG=Hs.273415 aldolase A, fructose-bisphosphate
220532_s_at	gb:NM_014020.1 /DEF=Homo sapiens LR8 protein (LR8), mRNA. /FEA=mrna /GEN=LR8 /PROD=LR8 protein /DB_XREF=gi:7662497 /UG=Hs.190161
203987_at	LR8 protein /FL=gb:AF115384.1 gb:NM_014020.1
202658_at	gb:NM_001765.1 /DEF=Homo sapiens CD1C antigen, c polypeptide (CD1C), mRNA. /FEA=mrna /GEN=CD1C /PROD=CD1C antigen, c polypeptide /DB_XREF=gi:4502646 /UG=Hs.1311 CD1C antigen, c polypeptide /FL=gb:M28827.1 gb:NM_001765.1
200991_s_at	.1 /DEF=Homo sapiens peroxisomal biogenesis factor 11B (PEX11B), mRNA. /FEA=mrna /GEN=PEX11B /PROD=peroxisomal biogenesis factor 11B /DB_XREF=gi:4505718 /UG=Hs.83023 peroxisomal biogenesis factor 11B /FL=gb:AF093670.1 gb:AB018080.1
203007_s_at	gb:NM_003846.1
200991_s_at	gb:NM_014748.1 /DEF=Homo sapiens KIAA0064 gene product (KIAA0064), mRNA. /FEA=mrna /GEN=KIAA0064 /PROD=KIAA0064 gene product /DB_XREF=gi:7661889 /UG=Hs.278569 sorting nexin 17 /FL=gb:BC002524.1 gb:BC002610.1 gb:D31764.1 gb:NM_014748.1
203007_s_at	gb:AF267856.1 /DEF=Homo sapiens HT033 mRNA, complete cds. /FEA=mrna /PROD=HT033 /DB_XREF=gi:12006038 /UG=Hs.8084 hypothetical protein
213969_x_at	gb:AF267856.1 /FL=gb:AF247168.1 gb:AF267856.1
200094_s_at	Consensus includes gb:BF683426 /FEA=EST /DB_XREF=gi:11968834 /DB_XREF=est:602139603F1 /CLONE=IMAGE:4300777 /UG=Hs.183698 ribosomal protein L29
200929_x_at	Consensus includes gb:AI004246 /FEA=EST /DB_XREF=gi:3213756 /DB_XREF=est:ou03g06.x1 /CLONE=IMAGE:1625242 /UG=Hs.75309 eukaryotic translation elongation factor 2
203929_x_at	gb:BC004954.1 /DEF=Homo sapiens, clone MGC:10897, mRNA, complete cds. /FEA=mrna /PROD=Unknown (protein for MGC:10897) /DB_XREF=gi:13436331 /UG=Hs.180842 ribosomal protein L13 /FL=gb:BC000851.1 gb:BC004954.1 gb:NM_000977.1

206170_at	gb:NM_000024.2 /DEF=Homo sapiens adrenergic, beta-2-, receptor, surface (ADRB2), mRNA. /FEA=mrna /GEN=ADRB2 /PROD=adrenergic, beta-2-, receptor, surface /DB_XREF=gi:13162366 /UG=Hs.2551 adrenergic, beta-2-, receptor, surface /FL=gb:NM_000024.2 gb:M15169.1
212582_at	Consensus includes gb:AL049923.1 /DEF=Homo sapiens mRNA; CDNA DKFZp564E2282 (from clone DKFZp564E2282). /FEA=mrna /DB_XREF=gi:4884169 /UG=Hs.109694 KIAA1451 protein
208630_at	Consensus includes gb:A1972144 /FEA=EST /DB_XREF=gi:5768970 /DB_XREF=est:wr63b03.x1 /CLONE=IMAGE:2492333 /UG=Hs.75860 hydroxyl-Coenzyme A dehydrogenase3-ketoacyl-Coenzyme A thiolaseenoyl-Coenzyme A hydrolase (trifunctional protein), alpha subunit /FL=gb:NM_000182.1 gb:D16480.1 gb:U04627.1
214058_at	Consensus includes gb:M19720 /DEF=Human I-myc protein gene, complete cds /FEA=mrna_2 /DB_XREF=gi:188906 /UG=Hs.92137 v-myc avian myelocytomatosis viral oncogene homolog 1, lung carcinoma derived
201991_s_at	Consensus includes gb:BF223224 /FEA=EST /DB_XREF=gi:11130401 /DB_XREF=est:7q30g05.x1 /CLONE=IMAGE:3700017 /UG=Hs.149436 kinesin family member 5B /FL=gb:NM_004521.1
212179_at	Consensus includes gb:AW157501 /FEA=EST /DB_XREF=gi:6228902 /DB_XREF=est:au83a02.x1 /CLONE=IMAGE:2782826 /UG=Hs.18368 DKFZP564B0769 protein
210949_s_at	gb:BC000533.1 /DEF=Homo sapiens, Similar to eukaryotic translation initiation factor 3, subunit 8 (110kd), clone MGC:8693, mRNA, complete cds. /FEA=mrna /PROD=Similar to eukaryotic translation initiation factor 3, subunit 8 (110kd) /DB_XREF=gi:12653522 /UG=Hs.4835 eukaryotic translation initiation factor 3, subunit 8 (110kd) /FL=gb:BC000533.1
213142_x_at	Consensus includes gb:AV700415 /FEA=EST /DB_XREF=gi:10302386 /DB_XREF=est:AV700415 /CLONE=GKCDGA04 /UG=Hs.12969 hypo-thetical protein
217817_at	Consensus includes gb:BR891920 /FEA=EST /DB_XREF=gi:10351728 /DB_XREF=est:601435490F1 /CLONE=IMAGE:3920590 /UG=Hs.323342 actin related protein 23 complex, subunit 4 (20 kd) /FL=gb:AF006087.1 gb:NM_005718.1
216041_x_at	Consensus includes gb:AK023348.1 /DEF=Homo sapiens cDNA FLJ13286 fis, Clone OVARC1001154, highly similar to Homo sapiens clone 24720 epithelin 1 and 2 mRNA. /FEA=mrna /DB_XREF=gi:10435243 /UG=Hs.180577 granulin
202687_s_at	gb:U57059.1 /DEF=Homo sapiens Apo-2 ligand mRNA, complete cds. /FEA=mrna /PROD=Apo-2 ligand /DB_XREF=gi:1336207 /UG=Hs.83429 tumor necrosis factor (ligand) superfamily, member 10 /FL=gb:U37518.1 gb:U57059.1 gb:NM_003810.1
215230_x_at	Consensus includes gb:AA679705 /FEA=EST /DB_XREF=gi:2660227 /DB_XREF=est:ah15e04.s1 /CLONE=IMAGE:1156734 /UG=Hs.4835 eukaryotic translation initiation factor 3, subunit 8 (110kd)
200647_x_at	gb:NM_003752.2 /DEF=Homo sapiens eukaryotic translation initiation factor 3, subunit 8 (110kd) (EIF3S8), mRNA. /FEA=mrna /GEN=EIF3S8 /PROD=eukaryotic translation initiation factor 3, subunit 8 (110kd) /DB_XREF=gi:5579457 /UG=Hs.4835 eukaryotic translation initiation factor 3, subunit 8 (110kd) /FL=gb:NM_003752.2
200078_s_at	gb:BC005876.1 /DEF=Homo sapiens, ATPase, H+ transporting, lysosomal (vacuolar proton pump) 21kd, clone MGC:4498, mRNA, complete cds. /FEA=mrna /PROD=ATPase, H+ transporting, lysosomal (vacuolar proton pump) 21kd /DB_XREF=gi:13543437 /FL=gb:BC005876.1
202169_s_at	gb:AF302110.1 /DEF=Homo sapiens alpha-aminoadipic semialdehyde dehydrogenase-phosphopantetheinyl transferase mRNA, complete cds. /FEA=mrna /PROD=alpha-aminoadipic semialdehyde dehydrogenase-phosphopantetheinyl transferase /DB_XREF=gi:11120434 /UG=Hs.64595 aminoadipate-semialdehyde dehydrogenase-phosphopantetheinyl transferase /FL=gb:AF302110.1 gb:AF136978.1 gb:AF151838.1 gb:AF151057.1 gb:NM_015423.1 gb:AF201943.1
202659_at	gb:NM_002801.1 /DEF=Homo sapiens proteasome (prosome, macropain) subunit, beta type, 10 (PSMB10), mRNA. /FEA=mrna /GEN=PSMB10 /PROD=proteasome (prosome, macropain) subunit, beta type, 10 /DB_XREF=gi:4506190 /UG=Hs.9661 proteasome (prosome, macropain) subunit, beta type, 10 /FL=gb:NM_002801.1
221488_s_at	gb:AF230924.1 /DEF=Homo sapiens brain acetylcholinesterase putative membrane anchor mRNA, complete cds. /FEA=mrna /PROD=brain acetylcholinesterase putative membrane anchor /DB_XREF=gi:7341254 /UG=Hs.107187 divalent cation tolerant protein CUTA /FL=gb:AF230924.1
221622_s_at	gb:AF246240.1 /DEF=Homo sapiens HT026 mRNA, complete cds. /FEA=mrna /PROD=HT026 /DB_XREF=gi:12005514 /UG=Hs.24371 uncharacterized hypothalamus protein HT007 /FL=gb:AF246240.1

206050_s_at	gb:NM_002939.1 /DEF=Homo sapiens ribonucleaseangiogenin inhibitor (RNH), mRNA. /FEA=mrna /GEN=RNH /PROD=ribonucleaseangiogenin
212199_at	Consensus includes gb:AL566962 /FEA=EST /DB_XREF=gi:12919867 /DB_XREF=est:AL566962 /CLONE=CS0DF026YH08 (3 prime) /UG=Hs.284281 Human putative ribosomal protein S1 mRNA
201861_s_at	Consensus includes gb:B9965566 /FEA=EST /DB_XREF=gi:1232781 /DB_XREF=est:602277032F1 /CLONE=IMAGE:4364790 /UG=Hs.326159 leucine rich repeat (in FLII) interacting protein 1 /FL=gb:NM_004735.1
212795_at	Consensus includes gb:AL137753.1 /DEF=Homo sapiens mRNA; cDNA DKFZp434K1412 (from clone DKFZp434K1412). /FEA=mrna /DB_XREF=gi:6808455 /UG=Hs.12144 KIAA1033 protein
2123574_s_at	Consensus includes gb:AA861608 /FEA=EST /DB_XREF=gi:2933748 /DB_XREF=est:ak34e01.s1 /CLONE=IMAGE:1407864 /UG=Hs.180446 karyopherin (importin) beta 1
215171_s_at	Consensus includes gb:AK023063.1 /DEF=Homo sapiens cDNA FLJ13001 fis, clone NT2RP3000341, highly similar to Homo sapiens mitochondrial inner membrane preprotein translocase Timl7a mRNA, nuclear gene encoding mitochondrial protein. /FEA=mrna /DB_XREF=gi:10434808 /UG=Hs.20716 translocase of inner mitochondrial membrane 17 (yeast) homolog A
210137_s_at	gb:BC001286.1 /DEF=Homo sapiens, Similar to dCMP deaminase, clone MGC:5160, mRNA, complete cds. /FEA=mrna /PROD=Similar to dCMP deaminase /DB_XREF=gi:12654884 /UG=Hs.76894 dCMP deaminase /FL=gb:BC001286.1
2122943_at	Consensus includes gb:AB011100.2 /DEF=Homo sapiens mRNA for KIAA0528 protein, partial cds. /FEA=mrna /GEN=KIAA0528 /PROD=KIAA0528 protein /DB_XREF=gi:6683714 /UG=Hs.30656 KIAA0528 gene product
20202164_s_at	gb:AF180476.1 /DEF=Homo sapiens CALIFP (CALIF) mRNA, complete cds. /FEA=mrna /GEN=CALIF /PROD=CALIFP /DB_XREF=gi:6856208 /UG=Hs.26703 CCR4-NOT transcription complex, subunit 8 /FL=gb:AF053318.1 gb:NM_004779.1 gb:AL122045.1 gb:AF180476.1
20209005_at	gb:AF157323.1 /DEF=Homo sapiens p45SKP2-like protein mRNA, complete cds. /FEA=mrna /PROD=p45SKP2-like protein /DB_XREF=gi:7688696 /UG=Hs.5548 f-box and leucine-rich repeat protein 5 /FL=gb:AF199420.1 gb:AF142481.1 gb:AF157323.1
20202899_s_at	gb:NM_003017.1 /DEF=Homo sapiens splicing factor, arginineserine-rich 3 (SFRS3), mRNA. /FEA=mrna /GEN=SFRS3 /PROD=splicing factor, arginineserine-rich 3 /DB_XREF=gi:4506900 /UG=Hs.167460 splicing factor, arginineserine-rich 3 /FL=gb:LI10838.1 gb:NM_003017.1
20208777_s_at	gb:AF001212.1 /DEF=Homo sapiens 26S proteasome subunit 9 mRNA, complete cds. /FEA=mrna /PROD=26S proteasome subunit 9 /DB_XREF=gi:2150045 /UG=Hs.90744 proteasome (prosome, macropain) 26S subunit, non-ATPase, 11
21219889_at	FL=gb:BC000437.1 gb:BC004430.1 gb:AB003102.1 gb:AF001212.1 gb:NM_002815.1
20204961_s_at	gb:NM_005479.1 /DEF=Homo sapiens frequently rearranged in advanced T-cell lymphomas (FRAT1), mRNA. /FEA=mrna /GEN=FRAT1 /PROD=frequently rearranged in advanced T-cell lymphomas /DB_XREF=gi:4885246 /UG=Hs.126057 frequently rearranged in advanced T-cell lymphomas /FL=gb:U58975.2 gb:NM_005479.1
21717106_x_at	gb:NM_000265.1 /DEF=Homo sapiens neutrophil cytosolic factor 1 (47kD, chronic granulomatous disease, autosomal 1) (NCF1), mRNA.
212224_at	FEA=mrna /GEN=NCF1 /PROD=neutrophil cytosolic factor 1 /DB_XREF=gi:4557784 /UG=Hs.1583 neutrophil cytosolic factor 1 (47kD, chronic granulomatous disease, autosomal 1) /FL=gb:BC002816.1 gb:AF330627.1 gb:M55067.1 gb:M25665.1 gb:NM_000265.1
2204125_at	Consensus includes gb:AF091078.1 /DEF=Homo sapiens clone 559 unknown mRNA, complete sequence. /FEA=mrna /PROD=unknown /DB_XREF=gi:3859993 /UG=Hs.125819 putative dimethyladenosine transferase
2217752_s_at	Consensus includes gb:NM_000689.1 /DEF=Homo sapiens aldehyde dehydrogenase 1, soluble (ALDH1), mRNA. /FEA=CDS /GEN=ALDH1 /PROD=aldehyde dehydrogenase 1, soluble /DB_XREF=gi:4502030 /UG=Hs.76392 aldehyde dehydrogenase 1 family, member A1 /FL=gb:AF003341.1 gb:NM_000689.1
221087_s_at	gb:NM_016013.1 /DEF=Homo sapiens CGI-65 protein (LOC51103), mRNA. /FEA=mrna /GEN=LOC51103 /PROD=CGI-65 protein /DB_XREF=gi:7705778 /UG=Hs.106529 CGI-65 protein /FL=gb:BC000780.1 gb:AF151823.1 gb:NM_016013.1
	gb:NM_018235.1 /DEF=Homo sapiens hypothetical protein FLJ10830 (FLJ10830), mRNA. /FEA=mrna /GEN=FLJ10830 /PROD=hypothetical protein
	FLJ10830 /DB_XREF=gi:8922698 /UG=Hs.273230 hypothetical protein FLJ10830 /FL=gb:BC001375.1 gb:BC003176.1 gb:NM_018235.1
	gb:NM_014349.1 /DEF=Homo sapiens apolipoprotein L, 3 (APO13), mRNA. /FEA=mrna /GEN=APO13 /PROD=apolipoprotein L, 3

218139_s_at	/DB_XREF=gi:7656972 /UG=Hs.241535 apolipoprotein L, 3 /FL=gb:AY014905.1 gb:AF070675.1 gb:NM_014349.1
218139_s_at	gb:NM_018229.1 /DEF=Homo sapiens hypothetical protein FLJ10813 (FLJ10813), mRNA. /FEA=mrna /GEN=FLJ10813 /PROD=hypothetical protein FLJ10813 /DB_XREF=gi:8922687 /UG=Hs.106210 hypothetical protein FLJ10813
213878_at	Consensus includes gb:AI685944 /FEA=EST /DB_XREF=gi:4897238 /DB_XREF=est:tu38g02.x1 /CLONE=IMAGE:2253362 /UG=Hs.235069 RecQ protein-like (DNA helicase Q1-like)
201346_at	gb:NM_024551.1 /DEF=Homo sapiens hypothetical protein FLJ21432 (FLJ21432), mRNA. /FEA=mrna /GEN=FLJ21432 /PROD=hypothetical protein FLJ21432 /DB_XREF=gi:13375714 /UG=Hs.11641 hypothetical protein FLJ21432 /FL=gb:NM_024551.1 gb:BC004906.1
206874_s_at	Consensus includes gb:AL138761 /DEF=Human DNA sequence from clone RP11-16H23 on chromosome 10. Contains the gene KIAA0204 (HSLK) for a protein kinase, the COL17A1 gene for collagen type XVII alpha 1 (BP180), ESTs and GSSs /FEA=mrna_2 /DB_XREF=gi:8573811 /UG=Hs.105751 Ste20-related serine/threonine kinase /FL=gb:D86959.1 gb:NM_014720.1
221808_at	Consensus includes gb:NM_004251.1 /DEF=Homo sapiens RAB9, member RAS oncogene family (RAB9), mRNA. /FEA=CDS /GEN=RAB9 /PROD=RAB9, member RAS oncogene family /DB_XREF=gi:4759011 /UG=Hs.28726 RAB9, member RAS oncogene family /FL=gb:U44103.1 gb:NM_004251.1
211138_s_at	gb:BC005297.1 /DEF=Homo sapiens, Similar to kynurenine 3-monooxygenase (kynurenine 3-hydroxylase), clone MGC:12362, mRNA, complete cds. /FEA=mrna /PROD=Similar to kynurenine 3-monooxygenase (kynurenine 3-hydroxylase) /DB_XREF=gi:13529016 /UG=Hs.107318 kynurenine 3-monooxygenase (kynurenine 3-hydroxylase) /FL=gb:BC005297.1
201386_s_at	gb:AF279891.1 /DEF=Homo sapiens dead box protein 15 mRNA, complete cds. /FEA=mrna /PROD=dead box protein 15 /DB_XREF=gi:9624452 /UG=Hs.5683 DEADH (Asp-Glu-Ala-AspHis) box polypeptide 15 /FL=gb:AB001636.1 gb:NM_001358.1 gb:AF279891.1
203037_s_at	gb:NM_014751.1 /DEF=Homo sapiens KIAA0429 gene product (KIAA0429), mRNA. /FEA=mrna /GEN=KIAA0429 /PROD=KIAA0429 gene product /DB_XREF=gi:7662113 /UG=Hs.77694 KIAA0429 gene product /FL=gb:AB007889.1 gb:NM_014751.1
218356_at	gb:NM_013393.1 /DEF=Homo sapiens cell division protein FtsJ (FtsJ), mRNA. /FEA=mrna /GEN=FUH1 /PROD=cell division protein FtsJ /DB_XREF=gi:7019376 /UG=Hs.279877 cell division protein FtsJ /FL=gb:AF093415.1 gb:NM_013393.1
204405_x_at	gb:NM_014473.1 /DEF=Homo sapiens putative dimethyladenosine transferase (HSA9761), mRNA. /FEA=mrna /GEN=HSA9761 /PROD=putative dimethyladenosine transferase /DB_XREF=gi:7657197 /UG=Hs.125819 putative dimethyladenosine transferase /FL=gb:AF102147.1 gb:NM_014473.1
201608_s_at	gb:NM_007062.1 /DEF=Homo sapiens nuclear phosphoprotein similar to S. cerevisiae PWP1 (PWP1), mRNA. /FEA=mrna /GEN=PWP1 /PROD=nuclear phosphoprotein similar to S. cerevisiae PWP1 /DB_XREF=gi:5902033 /UG=Hs.172589 nuclear phosphoprotein similar to S. cerevisiae PWP1 /FL=gb:BC001652.1 gb:L07758.1 gb:NM_007062.1
201569_s_at	gb:NM_015380.1 /DEF=Homo sapiens CGI-51 protein (CGI-51), mRNA. /FEA=mrna /GEN=CGI-51 /PROD=CGI-51 protein /DB_XREF=gi:7661541 /UG=Hs.4877 CGI-51 protein /FL=gb:AF151809.1 gb:NM_015380.1
222244_s_at	Consensus includes gb:AK000749.1 /DEF=Homo sapiens cDNA FLJ20742 fis, clone HEP06891. /FEA=mrna /DB_XREF=gi:7021031 /UG=Hs.52184 hypothetical protein FLJ20618
201241_at	gb:NM_004939.1 /DEF=Homo sapiens DEADH (Asp-Glu-Ala-AspHis) box polypeptide 1 (DDX1), mRNA. /FEA=mrna /GEN=DDX1 /PROD=DEADH (Asp-Glu-Ala-AspHis) box polypeptide 1 /DB_XREF=gi:4826685 /UG=Hs.78580 DEADH (Asp-Glu-Ala-AspHis) box polypeptide 1
220731_s_at	gb:NM_018090.1 /DEF=Homo sapiens hypothetical protein FLJ10420 (FLJ10420), mRNA. /FEA=mrna /GEN=FLJ10420 /PROD=hypothetical protein FLJ10420 /DB_XREF=gi:8922415 /UG=Hs.289087 hypothetical protein FLJ10420 /FL=gb:NM_018090.1
208799_at	gb:BC004146.1 /DEF=Homo sapiens, proteasome (prosome, macropain) subunit, beta type, 5, clone MGC:2175, mRNA, complete cds.

	/FEA=mrna /PROD=proteasome (prosome, macropain) subunit, betatype, 5 /DB_XREF=gi:13278740 /UG=Hs.78596 proteasome (prosome, macropain) subunit, beta type, 5 /FL=gb:BC004146.1 gb:NM 002797.1 gb:D29011.1
221718_s_at	gb:H90360.1 /DEF=human type II cAMP-dependent protein kinase (Ht31) mRNA, complete cds. /FEA=CDS /GEN=Ht31 /PROD=protein kinase /DB_XREF=gi:184434 /FL=gb:M90360.1
208662_s_at	Consensus includes gb:AI885338 /FEA=EST /DB_XREF=gi:5590502 /DB_XREF=est:w192e09.x1 /CLONE=IMAGE:2432392 /UG=Hs.118174 tetratricopeptide repeat domain 3 /FL=gb:D84294.1
202118_s_at	Consensus includes gb:AA541758 /FEA=EST /DB_XREF=gi:2288192 /DB_XREF=est:ni87d05.s1 /CLONE=IMAGE:983817 /UG=Hs.14158 copine III /FL=gb:AB014536.1 gb:NM 003909.1 gb:AF07226.2
201740_at	gb:NM 004551.1 /DEF=Homo sapiens NADH dehydrogenase (ubiquinone) Fe-S protein 3 (30kD) (NADH-coenzyme Q reductase) (NDUFS3), mRNA. /FEA=mrna /GEN=NDUFS3 /PROD=NADH dehydrogenase (ubiquinone) Fe-S protein 3 (30kD) (NADH-coenzyme Q reductase) /DB_XREF=gi:4758787 /UG=Hs.5273 NADH dehydrogenase (ubiquinone) Fe-S protein 3 (30kD) (NADH-coenzyme Q reductase) /FL=gb:BC000617.1 gb:AF067139.1 gb:NM 004551.1 gb:AF100743.1
215952_s_at	Consensus includes gb:AF090094.1 /DEF=Homo sapiens clone IMAGE 172979. /FEA=mrna /DB_XREF=gi:4063629 /UG=Hs.125078 ornithine decarboxylase antizyme 1
212796_s_at	Consensus includes gb:BF195608 /FEA=EST /DB_XREF=gi:11082676 /DB_XREF=est:7n85f03.x1 /CLONE=IMAGE:35711349 /UG=Hs.126084 KIAA1055 protein
210561_s_at	gb:AI110243.1 /DEF=Homo sapiens mRNA; cDNA DKFZp564B0482 (from clone DKFZp564B0482); complete cds. /FEA=mrna /GEN=DKFZp564B0482 /PROD=hypothetical protein /DB_XREF=gi:5817189 /UG=Hs.187991 DKFZp564A122 protein /FL=gb:AF072880.1 gb:AF106683.1 gb:AL110243.1 gb:AF112205.1 gb:AF069313.2
202220_at	gb:NM 014949.1 /DEF=Homo sapiens KIAA0907 protein (KIAA0907), mRNA. /FEA=mrna /GEN=KIAA0907 /PROD=KIAA0907 protein /DB_XREF=gi:7662371 /UG=Hs.24656 KIAA0907 protein /FL=gb:AB020714.1 gb:NM 014949.1
203739_at	gb:NM 006526.1 /DEF=Homo sapiens zinc finger protein 217 (ZNF217), mRNA. /FEA=mrna /GEN=ZNF217 /PROD=zinc finger protein 217
	/DB_XREF=gi:5730123 /UG=Hs.155040 zinc finger protein 217 /FL=gb:AF041259.1 gb:NM 006526.1
211036_x_at	gb:BC006301.1 /DEF=Homo sapiens, anaphase-promoting complex subunit 5, clone MGC:13295, mRNA, complete cds. /FEA=mrna /PROD=anaphase-promoting complex subunit 5 /DB_XREF=gi:13623410 /FL=gb:BC006301.1
204060_s_at	gb:NM 005044.1 /DEF=Homo sapiens protein kinase, X-linked (PRKX), mRNA. /FEA=mrna /GEN=PRKX /PROD=protein kinase, X-linked
64064_at	/DB_XREF=gi:4826947 /UG=Hs.147996 protein kinase, X-linked /FL=gb:NM 005044.1
	Cluster Incl. AI435089:th95b11.x1 Homo sapiens cDNA, 3 end /CLONE=IMAGE-2126397 /clone_end=3 /gb=AI435089 /gi=4300737 /ug=Hs.26194 /len=891
201515_s_at	gb:NM 004622.1 /DEF=Homo sapiens translin (TSN), mRNA. /FEA=mrna /GEN=TSN /PROD=translin /DB_XREF=gi:4759269 /UG=Hs.75066 translin /FL=gb:NM 004622.1
219093_at	gb:NM 017933.1 /DEF=Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mRNA. /FEA=mrna /GEN=FLJ20701 /PROD=hypothetical protein FLJ20701 /DB_XREF=gi:8923631 /UG=Hs.169764 hypothetical protein FLJ20701 /FL=gb:NM 017933.1
221739_at	Consensus includes gb:AL524093 /FEA=EST /DB_XREF=gi:12787586 /DB_XREF=est:AL524093 /CLONE=CS0DC002YI04 (5 prime) /UG=Hs.10927 hypothetical protein EUROMAGE1875335
208822_s_at	gb:U18321.1 /DEF=Human ionizing radiation resistance conferring protein mRNA, complete cds. /FEA=mrna /PROD=ionizing radiation resistance conferring protein /DB_XREF=gi:603763 /UG=Hs.159627 death associated protein 3 /FL=gb:U18321.1
218160_at	gb:NM 014222.1 /DEF=Homo sapiens NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 8 (19kD, PGIV) (NDUFA8), mRNA. /FEA=mrna /GEN=NDUFA8 /PROD=NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 8 (19kD, PGIV) /DB_XREF=gi:7657368 /UG=Hs.31547 NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 8 (19kD, PGIV) /FL=gb:BC001016.1 gb:AF044953.1
221728_x_at	Consensus includes gb:AA628440 /FEA=EST /DB_XREF=gi:2540827 /DB_XREF=est:af26f02.s1 /CLONE=IMAGE:1032795 /UG=Hs.83623 nuclear receptor subfamily 1, group I, member 3

210943_s_at	gb:U84744.1 /DEF=Human Chediak-Higashi syndrome protein short isoform (LYST) mRNA, complete cds. /FEA=mRNA /GEN=LYST /PROD=Chediak-Higashi syndrome protein short isoform /DB_XREF=gi:2654473 /UG=Hs.36508 Chediak-Higashi syndrome 1 /FL=gb:U84744.1
209104_s_at	gb:BC000009.1 /DEF=Homo sapiens, likely homolog of yeast Nhp2, component of the HACA snoRNP; hypothetical protein FLJ20479, clone MGC:1038, mRNA, complete cds. /FEA=mRNA /PROD=likely homolog of yeast Nhp2, component of the HACA snoRNP; hypothetical protein FLJ20479 /DB_XREF=gi:12652540 /UG=Hs.23990 nucleolar protein family A, member 2 (HACA small nucleolar RNPs) /FL=gb:BC000009.1 gb:NM 017838.1
217987_at	gb:NM_019048.1 /DEF=Homo sapiens hypothetical protein (FLJ20752), mRNA. /FEA=mRNA /GEN=FLJ20752 /PROD=hypothetical protein tein
201699_at	/DB_XREF=gi:9506696 /UG=Hs.101364 hypothetical protein /FL=gb:BC001243.1 gb:NM 019048.1 /GEN=P5MC6
201359_at	/PROD=proteasome (prosome, macropain) 26S subunit, ATPase, 6 /DB_XREF=gi:4506214 /UG=Hs.79357 proteasome (prosome, macropain) 26S subunit, ATPase, 6 /FL=gb:BC005390.1 gb:D78275.1 gb:AF006305.1 gb:NM 002806.1
210027_s_at	gb:NM_016451.1 /DEF=Homo sapiens coatomer protein complex, subunit beta (COPB), mRNA. /FEA=mRNA /GEN=COPB /PROD=coatomer protein complex, subunit beta /DB_XREF=gi:7705368 /UG=Hs.3059 coatomer protein complex, subunit beta /FL=gb:AF084457.1 gb:AL136593.1 gb:NM 016451.1
202096_s_at	gb:M80261.1 /DEF=Human apurinic endonuclease (APE) mRNA, complete cds. /FEA=mRNA /GEN=APE /PROD=apurinic endonuclease /DB_XREF=gi:178742 /UG=Hs.73722 APEX nuclease (multifunctional DNA repair enzyme) /FL=gb:BC004979.1 gb:M80261.1
214948_s_at	gb:NM_000714.2 /DEF=Homo sapiens benzodiazepine receptor (peripheral) (BZRP), nuclear gene encoding mitochondrial protein, transcript variant PBR, mRNA. /FEA=mRNA /GEN=BZRP /PROD=peripheral benzodiazepine receptor /DB_XREF=gi:6382068 /UG=Hs.202 benzodiazepine receptor (peripheral) /FL=gb:BC001110.1 gb:M36035.1 gb:NM 000714.2
200042_at	Consensus includes gb:AL050136.1 /DEF=Homo sapiens mRNA; cDNA DKFp586L141 (from clone DKFp586L141). /FEA=mRNA /DB_XREF=gi:4884346 /UG=Hs.140945 Homo sapiens mRNA; cDNA DKFp586L141 (from clone DKFp586L141) /gb:NM 014306.1 /DEF=Homo sapiens hypothetical protein (HSPC117), mRNA. /FEA=mRNA /GEN=HSPC117 /PROD=similar to C. elegans hypothetical 55.2 kD protein F16A11.2 /DB_XREF=gi:7657014 /UG=Hs.10729 hypothetical protein /FL=gb:BC000151.1 gb:BC002970.1 gb:AF161466.1 gb:NM 014306.1 gb:AF155658.1
219035_s_at	gb:NM_025126.1 /DEF=Homo sapiens hypothetical protein FLJ21786 (FLJ21786), mRNA. /FEA=mRNA /GEN=FLJ21786 /PROD=hypothetical protein FLJ21786 /DB_XREF=gi:13376704 /UG=Hs.316809 hypothetical protein FLJ21786 /FL=gb:NM 025126.1
200041_s_at	gb:NM_004640.1 /DEF=Homo sapiens HLA-B associated transcript-1 (D6S81E), mRNA. /FEA=mRNA /GEN=D6S81E /PROD=HLA-B associated
216321_s_at	transcript-1 /DB_XREF=gi:4758111 /UG=Hs.55296 HLA-B associated transcript-1 /FL=gb:BC004350.1 gb:NM 004640.1
214574_x_at	Consensus includes gb:X03348.1 /DEF=Human mRNA for beta-glucocorticoid receptor (clone OB10). /FEA=mRNA /PROD=beta-glucocorticoid receptor /DB_XREF=gi:31681 /UG=Hs.75772 nuclear receptor subfamily 3, group C, member 1
205370_x_at	Consensus includes gb:NM_007161.1 /DEF=Homo sapiens DNA segment on chromosome 6 (unique) 49 expressed sequence, NK cell triggering receptor, p30 (D6S49E), mRNA. /FEA=CDS /GEN=D6S49E /PROD=leukocyte-specific transcript 1 /DB_XREF=gi:6005740 /UG=Hs.88411 lymphocyte antigen 117 /FL=gb:NM 007161.1
213872_at	gb:NM_001918.1 /DEF=Homo sapiens dihydrolipoamide branched chain transacylase (E2 component of branched chain keto acid dehydrogenase complex; maple syrup urine disease) (DBT), mRNA. /FEA=mRNA /GEN=BDT /PROD=dihydrolipoamide branched chain transacylase (E2 component of branched chain keto acid dehydrogenase complex; maple syrup urine disease) /DB_XREF=gi:4503264 /UG=Hs.139410 dihydrolipoamide branched chain transacylase (E2 component of branched chain keto acid dehydrogenase complex; maple syrup urine disease) /FL=gb:J03208.1 gb:NM 001918.1 gb:M27093.1
	Consensus includes gb:BE465032 /FEA=EST /DB_XREF=gi:9510807 /DB_XREF=est:hv76g09.x1 /CLONE=IMAGS:3179392

	/UG=Hs.173685 hypothetical protein FLJ12619
201576_s_at	gb:NM_000404.1 /DEF=Homo sapiens galactosidase, beta 1 (GLB1), mRNA. /FEA=mrna /GEN=GLB1 /PROD=galactosidase, beta 1 /DB_XREF=gi:10834965 /UG=Hs.79222 galactosidase, beta 1 /FL=gb:NM_000404.1 gb:M27507.1 gb:M22590.1 gb:M34423.1
202548_s_at	gb:NM_003899.1 /DEF=Homo sapiens PAK-interacting exchange factor beta (P85SPR), mRNA. /FEA=mrna /GEN=P85SPR /PROD=PAK-interacting exchange factor beta /DB_XREF=gi:4505572 /UG=Hs.172813 PAK-interacting exchange factor beta /FL=gb:D63476.1 gb:NM_003899.1
204028_s_at	gb:NM_012197.2 /DEF=Homo sapiens rab6 GTPase activating protein (GAP and centrosome-associated) (GAPCENA), mRNA. /FEA=mrna /GEN=GAPCENA /PROD=rab6 GTPase activating protein (GAP and centrosome-associated) /DB_XREF=gi:12232372 /UG=Hs.55099 rab6 GTPase activating protein (GAP and centrosome-associated) /FL=gb:NM_012197.2
202435_s_at	Consensus includes gb:AV154504 /FEA=EST /DB_XREF=gi:11016025 /DB_XREF=est:AV154504 /CLONE=NT2RP4001328 /UG=Hs.154654 cytochrome P450, subfamily I (dioxin-inducible), polypeptide 1 (glaucoma 3, primary infantile) /FL=gb:NM_000104.2 gb:U03688.1
217980_s_at	gb:NM_017840.1 /DEF=Homo sapiens hypothetical protein FLJ20484 (FLJ20484), mRNA. /FEA=mrna /GEN=FLJ20484 /PROD=hypothetical protein FLJ20484 /DB_XREF=gi:8923447 /UG=Hs.5080 hypothetical protein FLJ20484 /FL=gb:AF275806.1 gb:BC001040.1 gb:NM_017840.1 gb:AF183428.1
201112_s_at	gb:NM_001316.1 /DEF=Homo sapiens chromosome segregation 1 (yeast homolog)-like (CSE1L), mRNA. /FEA=mrna /GEN=CSE1L /PROD=chromosome segregation 1 (yeast homolog)-like /DB_XREF=gi:4503072 /UG=Hs.90073 chromosome segregation 1 (yeast homolog)-like /FL=gb:U33286.1 gb:AF053641.1 gb:NM_001316.1
202322_s_at	gb:NM_004837.1 /DEF=Homo sapiens geranylgeranyl diphosphate synthase 1 (GGPS1), mRNA. /FEA=mrna /GEN=GGPS1 /PROD=geranylgeranyl diphosphate synthase 1 /DB_XREF=gi:4758429 /UG=Hs.55498 geranylgeranyl diphosphate synthase 1 /FL=gb:AF057698.1 gb:BC005252.1 gb:AB017971.1 gb:AB016043.1 gb:AB019036.1 gb:NM_004837.1 gb:AF125394.1
203545_at	gb:NM_024079.1 /DEF=Homo sapiens hypothetical protein MGC2840 similar to a putative glucosyltransferase (MGC2840), mRNA. /FEA=mrna /GEN=MGC2840 /PROD=hypothetical protein MGC2840 similar to a putative glucosyltransferase /DB_XREF=gi:13129069 /UG=Hs.155356 hypothetical protein MGC2840 similar to a putative glucosyltransferase /FL=gb:BC001133.1 gb:NM_024079.1
212646_at	Consensus includes gb:D42043.1 /DEF=Human mRNA for KIAA0084 gene, partial cds. /FEA=mrna /GEN=KIAA0084 /DB_XREF=gi:577298 /UG=Hs.79123 KIAA0084 protein
212591_at	Consensus includes gb:AA887480 /FEA=EST /DB_XREF=gi:3003168 /DB_XREF=est:oj54a12.s1 /CLONE=IMAGE:1502110 /UG=Hs.17428 RBP1-like protein
218005_at	Consensus includes gb:AA744771 /FEA=EST /DB_XREF=gi:2783535 /DB_XREF=est:ny71d07.s1 /CLONE=IMAGE:1283725 /UG=Hs.108642 zinc finger protein 22 (KOX 15) /FL=gb:NM_008963.1
201165_s_at	Consensus includes gb:BE670915 /FEA=EST /DB_XREF=gi:10031456 /DB_XREF=est:7e43a09.x1 /CLONE=IMAGE:3285208 /UG=Hs.153834 pumilio (Drosophila) homolog 1 /FL=gb:AF315592.1 gb:NM_014676.1
212239_at	Consensus includes gb:AI680192 /FEA=EST /DB_XREF=gi:4890374 /DB_XREF=est:tw66a10.x1 /CLONE=IMAGE:2264634 /UG=Hs.6241 phosphoinositide-3-kinase, regulatory subunit, polypeptide 1 (p85 alpha)
204386_s_at	Consensus includes gb:BF303597 /FEA=EST /DB_XREF=gi:11250218 /DB_XREF=est:60186230f2 /CLONE=IMAGE:4120446 /UG=Hs.182695 hypothetical protein MGC3243 /FL=gb:BC000002.1 gb:NM_024026.1
214853_s_at	Consensus includes gb:AI091079 /FEA=EST /DB_XREF=gi:3430138 /DB_XREF=est:qa53e05.s1 /CLONE=IMAGE:1690496 /UG=Hs.81972 SHC (Src homology 2 domain-containing) transforming protein 1
210580_x_at	gb:125275.1 /DEF=Human estrogen sulfotransferase mRNA, complete cds. /FEA=mrna /PROD=estrogen sulfotransferase /DB_XREF=gi:463124 /UG=Hs.274614 sulfotransferase family, cytosolic, 1A, phenol-prefering, member 3 /FL=gb:L25275.1
222150_s_at	Consensus includes gb:AK026747.1 /DEF=Homo sapiens cDNA: FLJ23094 fis, clone LNG07379, highly similar to HST000007 Homo sapiens
209265_s_at	mRNA full length insert cDNA clone EUROIMAGE 293605. /FEA=mrna /DB_XREF=gi:10439670 /UG=Hs.12969 hypothetical protein gb:BC001650.1 /DEF=Homo sapiens, Similar to putative methyltransferase, Clone MGC:2709, mRNA, complete cds. /FEA=mrna /PROD=Similar to putative methyltransferase /DB_XREF=gi:12804482 /UG=Hs.268149 putative methyltransferase /FL=gb:BC003031.1 gb:BC001650.1 gb:NM_019852.1

218807_at	gb:NM_006113.2 /DEF=Homo sapiens vav 3 oncogene (VAV3), mRNA. /FEA=mrna /GEN=VAV3 /PROD=vav 3 oncogene /DB_XREF=gi:7262390 /UG=Hs.267659 vav 3 oncogene /FL=gb:AF067817.1 gb:AF118887.1 gb:NM_006113.2
209043_at	gb:AF033026.1 /DEF=Homo sapiens bifunctional ATP sulfurylaseadenosine 5-phosphosulfate kinase mRNA, complete cds. /FEA=mrna /PROD=bifunctional ATP sulfurylaseadenosine5-phosphosulfate kinase /DB_XREF=gi:3378100 /UG=Hs.3833 3-phosphoadenosine 5-phosphosulfate synthase 1 /FL=gb:AF033026.1 gb:AF016496.1 gb:NM_005443.1 gb:AF105227.1
219777_at	gb:NM_024711.1 /DEF=Homo sapiens hypothetical protein FLJ22690 (FLJ22690), mRNA. /FEA=mrna /GEN=FLJ22690 /PROD=hypothetical protein FLJ22690 /UG=Hs.105468 hypothetical protein FLJ22690 /FL=gb:NM_024711.1
218048_at	gb:NM_012071.1 /DEF=Homo sapiens BUP protein (BUP), mRNA. /FEA=mrna /GEN=BUP /PROD=BUP protein /DB_XREF=gi:6912277 /UG=Hs.35660 BUP protein /FL=gb:AF078848.1 gb:AF201948.1 gb:NM_012071.1
201986_at	Consensus includes gb:AB011165.1 /DEF=Homo sapiens mRNA for KIAA0593 protein, partial cds. /FEA=mrna /GEN=KIAA0593 /PROD=KIAA0593 protein /DB_XREF=gi:3043709 /UG=Hs.11861 thyroid hormone receptor-associated protein, 240 kDa subunit /FL=gb:AF117754.1 gb:NM_005121.1
219799_s_at	gb:NM_005771.1 /DEF=Homo sapiens retinol dehydrogenase homolog (RDHL), mRNA. /FEA=mrna /GEN=RDHL /PROD=retinol dehydrogenase homolog /DB_XREF=gi:5032034 /UG=Hs.179608 retinol dehydrogenase homolog /FL=gb:AF067174.1 gb:NM_005771.1
208688_x_at	gb:U78525.1 /DEF=Homo sapiens eukaryotic translation initiation factor (eIF3) mRNA, complete cds. /FEA=mrna /GEN=eIF3 /PROD=eukaryotic translation initiation factor /DB_XREF=gi:2558667 /UG=Hs.57783 eukaryotic translation initiation factor 3, subunit 9 (eta, 116kD) /FL=gb:U78525.1
200001_at	gb:NM_001749.1 /DEF=Homo sapiens calpain 4, small subunit (30K) (CAPN4), mRNA. /FEA=mrna /GEN=CAPN4 /PROD=calpain 4 small subunit /DB_XREF=gi:4502564 /UG=Hs.74451 calpain 4, small subunit (30K) /FL=gb:BC000592.1 gb:NM_001749.1
218118_s_at	gb:NM_006327.1 /DEF=Homo sapiens translocase of inner mitochondrial membrane 23 (yeast) homolog (TIM23), mRNA. /FEA=mrna /GEN=TIM23 /PROD=translocase of inner mitochondrial membrane 23 (yeast) homolog /DB_XREF=gi:5454121 /UG=Hs.283684 translocase of inner mitochondrial membrane 23 (yeast) homolog /FL=gb:AF030162.1 gb:NM_006327.1
201840_at	gb:NM_006156.1 /DEF=Homo sapiens neural precursor cell expressed, developmentally down-regulated 8 (NEDD8), mRNA. /FEA=mrna /GEN=NEDD8 /PROD=neural precursor cell expressed, developmentally down-regulated 8 /DB_XREF=gi:5453759 /UG=Hs.75512 neural precursor cell expressed, developmentally down-regulated 8 /FL=gb:D23662.1 gb:NM_006156.1
38710_at	Cluster Incl. AL096714:Homo sapiens mRNA; cDNA DKFZp564E242 (from clone DKFZp564E242) /cds=UNKNOWN /gb=AL096714 /gi=5419847 /ug=Hs.108504 /len=1904
212287_at	Consensus includes gb:BF382924 /FEA=EST /DB_XREF=gi:11364313 /DB_XREF=est:601816985F1 /CLONE=IMAGE:4050909 /UG=Hs.197803 KIAA0160 protein
203098_at	Consensus includes gb:AL050164.1 /DEF=Homo sapiens mRNA; cDNA DKFZp586C1622 (from clone DKFZp586C1622); partial cds. /FEA=mrna /GEN=DKFZp586C1622 /PROD=hypothetical protein /DB_XREF=gi:4884378 /UG=Hs.16081 chromodomain protein, Y chromosome-like /FL=gb:AF081258.1 gb:AF081259.1 gb:NM_004824.1
218905_at	gb:NM_017864.1 /DEF=Homo sapiens hypothetical protein FLJ20530 (FLJ20530), mRNA. /FEA=mrna /GEN=FLJ20530 /PROD=hypothetical protein FLJ20530 /DB_XREF=gi:8923495 /UG=Hs.279521 hypothetical protein FLJ20530 /FL=gb:NM_017864.1
218303_x_at	gb:NM_016618.1 /DEF=Homo sapiens hypothetical protein (LOC51315), mRNA. /FEA=mrna /GEN=LOC51315 /PROD=hypothetical protein /DB_XREF=gi:7706155 /UG=Hs.5721 hypothetical protein /FL=gb:AF208845.1 gb:AF217520.1 gb:NM_016618.1
208705_s_at	Consensus includes gb:BG481972 /FEA=EST /DB_XREF=gi:13414251 /DB_XREF=est:602526894F1 /CLONE=IMAGE:4650406 /UG=Hs.286236 eukaryotic translation initiation factor 5 /FL=gb:AL080102.1
218715_at	gb:NM_018428.1 /DEF=Homo sapiens hepatocellular carcinoma-associated antigen 66 (HCA66), mRNA. /FEA=mrna /GEN=HCA66 /PROD=hepatocellular carcinoma-associated antigen 66 /DB_XREF=gi:8923721 /UG=Hs.30670 hepatocellular carcinoma-associated antigen 66 /FL=gb:AF244135.1 gb:AF116631.1 gb:NM_018428.1
202184_s_at	gb:NM_018230.1 /DEF=Homo sapiens hypothetical protein FLJ10814 (FLJ10814), mRNA. /FEA=mrna /GEN=FLJ10814

	/PROD=hypothetical protein FLJ10814 /DB_XREF=gi:8922689 /UG=Hs.12457 hypothetical protein FLJ10814 /FL=gb:NM_018230.1
202004_x_at	gb:NM_003001.2 /DEF=Homo sapiens succinate dehydrogenase complex, subunit C, integral membrane protein, 15kd (SDHC), nuclear gene encoding mitochondrial protein, mRNA. /FEA=mrna /GEN=SDHC /PROD=succinate dehydrogenase complex, subunit C precursor /DB_XREF=gi:9257243 /UG=Hs.3577 succinate dehydrogenase complex, subunit C, integral membrane protein, 15kd /FL=gb:U57877.1 gb:NM_003001.2
209435_s_at	gb:BC000265.1 /DEF=Homo sapiens, clone MGC:3182, mRNA, complete cds. /FEA=mrna /PROD=Unknown (protein for MGC:3182) /DB_XREF=gi:12653008 /UG=Hs.315417 Homo sapiens, clone MGC:3182, mRNA, complete cds /FL=gb:BC000265.1
221044_s_at	gb:NM_021616.1 /DEF=Homo sapiens ring finger protein 21, interferon-responsive (RNF21), mRNA. /FEA=mrna /GEN=RNF21 /PROD=ring finger protein 21, interferon-responsive /DB_XREF=gi:11055977 /UG=Hs.125300 ring finger protein 21, interferon-responsive /FL=gb:AB039903.1 gb:NM_021616.1
200992_at	Consensus includes gb:AL137335.1 /DEF=Homo sapiens mRNA; cDNA DKFZp434A179 (from clone DKFZp434A179); partial cds. /FEA=mrna /GEN=DKFZp434A179 /PROD=hypothetical protein /DB_XREF=gi:6807827 /UG=Hs.5151 RAN binding protein 7 /FL=gb:AF098799.1 gb:NM_006391.1
201900_s_at	gb:NM_006066.1 /DEF=Homo sapiens aldo-keto reductase family 1, member A1 (aldehyde reductase) (AKR1A1), mRNA. /FEA=mrna /GEN=AKR1A1 /PROD=aldo-keto reductase family 1, member A1 (aldehyde reductase) /DB_XREF=gi:5174390 /UG=Hs.89529 aldo-keto reductase family 1, member A1 (aldehyde reductase) /FL=gb:BC000670.1 gb:NM_006066.1
202560_s_at	gb:NM_015607.1 /DEF=Homo sapiens DKFZP547E1010 protein (DKFZP547E1010), mRNA. /FEA=mrna /GEN=DKFZP547E1010 /PROD=DKFZP547E1010 protein /DB_XREF=gi:7661589 /UG=Hs.323817 DKFZP547E1010 protein /FL=gb:NM_015607.1
201105_at	gb:NM_002305.2 /DEF=Homo sapiens lectin, galactoside-binding, soluble, 1 (galectin 1) (LGALS1), mRNA. /FEA=mrna /GEN=LGALS1 /PROD=beta-galactosidase binding lectin precursor /DB_XREF=gi:6006015 /UG=Hs.227751 lectin, galactoside-binding, soluble, 1 (galectin 1) /FL=gb:BC001693.1 gb:J04456.1 gb:NM_002305.2
204546_at	gb:NM_014732.1 /DEF=Homo sapiens KIAA0513 gene product (KIAA0513), mRNA. /FEA=mrna /GEN=KIAA0513 /PROD=KIAA0513 gene product /DB_XREF=gi:7662163 /UG=Hs.301658 KIAA0513 gene product /FL=gb:AB011085.1 gb:NM_014732.1
214181_x_at	Consensus includes gb:AI735692 /FEA=EST /DB_XREF=gi:5057216 /DB_XREF=est:at20b12.x1 /CLONE=IMAGE:2355647 /UG=Hs.88411 lymphocyte antigen 117
219032_x_at	gb:NM_014322.1 /DEF=Homo sapiens opsin 3 (encephalopsin) (OPN3), mRNA. /FEA=mrna /GEN=OPN3 /PROD=opsin 3 (encephalopsin) /DB_XREF=gi:7657070 /UG=Hs.279926 opsin 3 (encephalopsin) /FL=gb:AF140242.1 gb:NM_014322.1
205306_x_at	Consensus includes gb:AI074145 /FEA=EST /DB_XREF=gi:3400789 /DB_XREF=est:ovl3a06.x1 /CLONE=IMAGE:1637170 /UG=Hs.107318 kynurenine 3-monooxygenase (kynurenine 3-hydroxylase) /FL=gb:AF056032.1 gb:NM_003679.1
202837_at	gb:NM_006700.1 /DEF=Homo sapiens FLN29 gene product (FLN29), mRNA. /FEA=mrna /GEN=FLN29 /PROD=FLN29 gene product /DB_XREF=gi:5729827 /UG=Hs.5148 FLN29 gene product /FL=gb:BC003553.1 gb:AB007447.1 gb:NM_006700.1
202153_s_at	gb:NM_016553.1 /DEF=Homo sapiens hypothetical protein (DKFZp547L134), mRNA. /FEA=mrna /GEN=DKFZp547L134 /PROD=hypothetical protein /DB_XREF=gi:7705354 /UG=Hs.9877 hypothetical protein /FL=gb:AL162061.1 gb:NM_016553.1
209341_s_at	Consensus includes gb:AUI53366 /FEA=EST /DB_XREF=gi:11014887 /DB_XREF=est:AUI53366 /CLONE=WT2RF3002988 /UG=Hs.226573 inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase beta /FL=gb:AF031416.1 gb:AF080158.1
212493_s_at	Consensus includes gb:AI761110 /FEA=EST /DB_XREF=gi:5176777 /DB_XREF=est:wi69h02.x1 /CLONE=IMAGE:2398611 /UG=Hs.6947 HSPC069 protein
201600_at	gb:NM_007273.1 /DEF=Homo sapiens B-cell associated protein (REA), mRNA. /FEA=mrna /GEN=REA /PROD=B-cell associated protein /DB_XREF=gi:6005853 /UG=Hs.7771 B-cell associated protein /FL=gb:AF150962.1 gb:NM_007273.1 gb:AF156021.1 gb:AF178980.1
201144_s_at	gb:NM_004094.1 /DEF=Homo sapiens eukaryotic translation initiation factor 2, subunit 1 (alpha, 35kd) (EIF2S1), mRNA. /FEA=mrna /GEN=EIF2S1 /PROD=eukaryotic translation initiation factor 2, subunit 1 (alpha, 35kd) /DB_XREF=gi:4758255 /UG=Hs.151777 eukaryotic translation initiation factor 2, subunit 1 (alpha, 35kd) /FL=gb:BC002513.1 gb:J02645.1
211985_s_at	gb:NM_004094.1 Consensus includes gb:AI653730 /FEA=EST /DB_XREF=gi:4737709 /DB_XREF=est:wb36f12.x1 /CLONE=IMAGE:2307791 /UG=Hs.279009 matrix Gla protein

201226_at	gb:NM 005004.1 /DEF=Homo sapiens NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 8 (19kD, ASH1) (NDUFB8), mRNA. /FEA=mRNA /GEN=NDUFB8 /PROD=NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 8 (19kD, ASH1) /DB_XREF=gi:4826853 /UG=Hs.198273 NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 8 (19kD, ASH1) /FL=gb:BC000466.1 gb:AF044958.1 gb:AF077028.1 gb:NM 005004.1 gb:AL080056.1
208828_at	gb:BC004170.1 /DEF=Homo sapiens, histone fold protein CHRAC17; DNA polymerase epsilon p17 subunit, clone MGC:2725, mRNA, complete cds. /FEA=mRNA /PROD=histone fold protein CHRAC17; DNA polymerase epsilon p17 subunit /DB_XREF=gi:13278800 /UG=Hs.108112 histone fold protein CHRAC17; DNA polymerase epsilon p17 subunit /FL=gb:BC003166.1 gb:BC004170.1 gb:AF226077.1 gb:NM 017443.1
204020_at	Consensus includes gb:BF739943 /FEA=EST /DB_XREF=gi:12066607 /DB_XREF=est:7041b04.x1 /CLONE=IMAGE:3576534 /UG=Hs.29117 purine-rich element binding protein A /FL=gb:M96684.1 gb:NM 005859.1
217942_at	gb:NM 021821.1 /DEF=Homo sapiens MDS023 protein (MDS023), mRNA. /FEA=mRNA /GEN=MDS023 /PROD=MDS023 protein /DB_XREF=gi:11141894 /UG=Hs.10724 MDS023 protein /FL=gb:AF182422.1 gb:NM 021821.1
203514_at	Consensus includes gb:BF971923 /FEA=EST /DB_XREF=gi:12339138 /DB_XREF=est:602240326f1 /CLONE=IMAGE:4328791 /UG=Hs.29282 mitogen-activated protein kinase kinase 3 /FL=gb:U78876.1 gb:NM 002401.1
204334_at	Consensus includes gb:AA488672 /FEA=EST /DB_XREF=gi:2216103 /DB_XREF=est:ab40d10.s1 /CLONE=IMAGE:843283 /UG=Hs.21599 Kruppel-like factor 7 (ubiquitous) /FL=gb:AB015132.1 gb:NM 003709.1
203531_at	Consensus includes gb:BF435809 /FEA=EST /DB_XREF=gi:11448124 /DB_XREF=est:nab42a09.x1 /CLONE=IMAGE:3268504 /UG=Hs.101299 cullin 5 /FL=gb:AF327710.1 gb:AF017061.1 gb:NM 003478.1
205022_s_at	gb:NM 005197.1 /DEF=Homo sapiens checkpoint suppressor 1 (CHES1), mRNA. /FEA=mRNA /GEN=CHES1 /PROD=checkpoint suppressor 1 /DB_XREF=gi:4885136 /UG=Hs.211773 checkpoint suppressor 1 /FL=gb:U68723.1 gb:NM 005197.1
201532_at	gb:NM 002788.1 /DEF=Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 3 (PSMA3), mRNA. /FEA=mRNA /GEN=PSMA3 /PROD=proteasome (prosome, macropain) subunit, alpha type, 3 /FL=gb:BC005265.1 gb:NM 002788.1
204972_at	gb:NM 016817.1 /DEF=Homo sapiens 2-Soligoadenylate synthetase 2 (OAS2), transcript variant 1, mRNA. /FEA=mRNA /GEN=OAS2 /PROD=2-Soligoadenylate synthetase 2, isoform p17 /DB_XREF=gi:8051624 /UG=Hs.264981 2-Soligoadenylate synthetase 2 /FL=gb:M87434.1 gb:NM 016817.1
209200_at	Consensus includes gb:AL536517 /FEA=EST /DB_XREF=gi:12800010 /DB_XREF=est:AL536517 /CLONE=CS0DF038YH13 (5 prime) /UG=Hs.78995 MADS box transcription enhancer factor 2, polypeptide C (myocyte enhancer factor 2C) /FL=gb:L08895.1
217945_at	gb:NM 025238.1 /DEF=Homo sapiens BTB (POZ) domain containing 1 (BTBD1), mRNA. /FEA=mRNA /GEN=BTBD1 /PROD=BTB (POZ) domain containing 1 /DB_XREF=gi:13376847 /UG=Hs.21332 BTB (POZ) domain containing 1 /FL=gb:AL136853.1 gb:AF257241.1 gb:NM 025238.1 gb:AF355402.1
201491_at	gb:NM 012111.1 /DEF=Homo sapiens chromosome 14 open reading frame 3 (C14ORF3), mRNA. /FEA=mRNA /GEN=C14ORF3 /PROD=chromosome 14 open reading frame 3 /DB_XREF=gi:6912279 /UG=Hs.204041 chromosome 14 open reading frame 3 /FL=gb:BC000321.1 gb:NM 012111.1 gb:AF164791.1
204868_at	gb:NM 001545.1 /DEF=Homo sapiens immature colon carcinoma transcript 1 (ICT1), mRNA. /FEA=mRNA /GEN=ICT1 /PROD=immature colon carcinoma transcript 1 /DB_XREF=gi:4557656 /UG=Hs.9078 immature colon carcinoma transcript 1 /FL=gb:NM 001545.1
217826_s_at	gb:NM 016021.1 /DEF=Homo sapiens CGI-76 protein (LOC51632), mRNA. /FEA=mRNA /GEN=LOC51632 /PROD=CGI-76 protein /DB_XREF=gi:7706311 /UG=Hs.184325 CGI-76 protein /FL=gb:AF151834.1 gb:AF161502.1 gb:AF151039.1 gb:NM 016021.1
212534_at	Consensus includes gb:AU144066 /FEA=EST /DB_XREF=gi:11005587 /DB_XREF=est:AU144066 /CLONE=HEMBA1000798 /UG=Hs.285519 Homo sapiens cDNA FLJ11904 f1s, clone HEMBB1000048
211284_s_at	gb:BC000324.1 /DEF=Homo sapiens, similar to granulin, clone MGC:8480, mRNA, complete cds. /FEA=mRNA /PROD=Similar to granulin /DB_XREF=gi:12653114 /UG=Hs.180577 granulin /FL=gb:BC000324.1
212188_at	Consensus includes gb:AA551075 /FEA=EST /DB_XREF=gi:2321327 /DB_XREF=est:nk74h06.s1 /CLONE=IMAGE:1019291 /UG=Hs.109438 Homo sapiens clone 24775 mRNA sequence

201458_s_at	gb:NM_004725.1 /DEF=Homo sapiens BUB3 (budding uninhibited by benzimidazoles 3, yeast) homolog (BUB3), mRNA. /FEA=mRNA /GEN=BUB3 /PROD=BUB3 (budding uninhibited by benzimidazoles 3, yeast) homolog /DB_XREF=gi:4757879 /UG=Hs.40323 BUB3 (budding uninhibited by benzimidazoles 3, yeast) homolog /FL=gb:BC005138.1 gb:AF047472.1 gb:AF053304.1 gb:AF081496.1 gb:NM_004725.1
201773_at	gb:NM_015339.1 /DEF=Homo sapiens activity-dependent neuroprotective protein (ADNP), mRNA. /FEA=mRNA /GEN=ADNP /PROD=activity-dependent neuroprotective protein /DB_XREF=gi:12229216 /UG=Hs.3657 activity-dependent neuroprotective protein /FL=gb:AF250860.1 gb:NM_015339.1
218751_s_at	gb:NM_018315.1 /DEF=Homo sapiens hypothetical protein FLJ11071 (FLJ11071), mRNA. /FEA=mRNA /GEN=FLJ11071 /PROD=hypothetical protein FLJ11071 /DB_XREF=gi:8922851 /UG=Hs.31945 hypothetical protein FLJ11071 /FL=gb:NM_018315.1
201350_at	gb:NM_004475.1 /DEF=Homo sapiens flotillin 2 (FLOT2), mRNA. /FEA=mRNA /GEN=FLOT2 /PROD=flotillin 2 /DB_XREF=gi:4758393 /UG=Hs.184488 flotillin 2 FL=gb:NM_004475.1 gb:M60922.1
201098_at	gb:NM_004766.1 /DEF=Homo sapiens coatomer protein complex, subunit beta 2 (beta prime), mRNA. /FEA=mRNA /GEN=COPB2 /PROD=coatomer protein complex, subunit beta 2 (beta prime) /DB_XREF=gi:4758031 /UG=Hs.75724 coatomer protein complex, subunit beta 2 (beta prime) /FL=gb:BC000326.1 gb:NM_004766.1
203732_at	gb:NM_016213.1 /DEF=Homo sapiens thyroid hormone receptor interactor 4 (TRIP4), mRNA. /FEA=mRNA /GEN=TRIP4 /PROD=activating signal cointegrator 1 /DB_XREF=gi:7706430 /UG=Hs.116784 thyroid hormone receptor interactor 4 /FL=gb:AF168418.1 gb:NM_016213.1
202846_s_at	gb:NM_002642.1 /DEF=Homo sapiens phosphatidylinositol glycan, class C (PIGC), mRNA. /FEA=mRNA /GEN=PIGC /PROD=phosphatidylinositol glycan, class C /DB_XREF=gi:4505794 /UG=Hs.75790 phosphatidylinositol glycan, class C /FL=gb:D85418.1 gb:NM_002642.1
205936_s_at	gb:NM_002115.1 /DEF=Homo sapiens hexokinase 3 (white cell) (HK3), mRNA. /FEA=mRNA /GEN=HK3 /PROD=hexokinase 3 (white cell) /DB_XREF=gi:4504394 /UG=Hs.159237 hexokinase 3 (white cell) /FL=gb:U51333.1 gb:NM_002115.1
201209_at	gb:NM_004964.2 /DEF=Homo sapiens histone deacetylase 1 (HDAC1), mRNA. /FEA=mRNA /GEN=HDAC1 /PROD=histone deacetylase 1 /DB_XREF=gi:13128859 /UG=Hs.88556 histone deacetylase 1 /FL=gb:BC000301.1 gb:U50079.1 gb:NM_004964.2 gb:D50405.1
217798_at	Consensus includes gb:AL123426 /FEA=EST /DB_XREF=gi:3539192 /DB_XREF=est:qa49c09.x1 /CLONE=IMAGE:1690096 /UG=Hs.239720 CCR4-NOT transcription complex, subunit 2 /FL=gb:AF113226.1 gb:AF180473.1 gb:NM_014515.1
209455_at	Consensus includes gb:BE963245 /FEA=EST /DB_XREF=gi:11766663 /DB_XREF=est:601656874R1 /CLONE=IMAGE:3865699 /UG=Hs.21229 f-box and WD-40 domain protein 1B /FL=gb:AF176022.1 gb:AB033281.1
212397_at	Consensus includes gb:AL137751.1 /DEF=Homo sapiens mRNA; cDNA DKFZp434I0812 (from clone DKFZp434I0812); partial cds. /FEA=mRNA /GEN=DKFZp434I0812 /PROD=hypothetical protein /DB_XREF=gi:6808387 /UG=Hs.263671 Homo sapiens mRNA; cDNA DKFZp434I0812 (from clone DKFZp434I0812); partial cds
218025_s_at	gb:NM_006117.1 /DEF=Homo sapiens peroxisomal D3, D2-enoyl-CoA isomerase (PECI), mRNA. /FEA=mRNA /GEN=PECI /PROD=peroxisomal D3, D2-enoyl-CoA isomerase /DB_XREF=gi:5174624 /UG=Hs.15250 peroxisomal D3, D2-enoyl-CoA isomerase /FL=gb:AL136642.1 gb:BC002668.1 gb:AF069301.1 gb:AF153612.1 gb:NM_006117.1 gb:AF244138.1
203217_s_at	gb:NM_003896.1 /DEF=Homo sapiens sialyltransferase 9 (CMP-NeuAc:lactosylceramide alpha-2,3-sialyltransferase; GM3 synthase) (SIAT9), mRNA. /FEA=mRNA /GEN=SIAT9 /PROD=sialyltransferase 9 (CMP-NeuAc:lactosylceramide alpha-2,3-sialyltransferase; GM3 synthase) /DB_XREF=gi:4506954 /UG=Hs.225939 sialyltransferase 9 (CMP-NeuAc:lactosylceramide alpha-2,3-sialyltransferase; GM3 synthase) /FL=gb:AB018356.1 gb:NM_003896.1 gb:AF119415.1
212812_at	Consensus includes gb:AF1700633 /FEA=EST /DB_XREF=gi:4988533 /DB_XREF=est:we38g03.x1 /CLONE=IMAGE:2343412 /UG=Hs.288232 Homo sapiens cDNA: FLJ22642 fis, clone HSI06970
207830_s_at	gb:NM_002713.1 /DEF=Homo sapiens protein phosphatase 1, regulatory (inhibitor) subunit 8 (PPP1R8), mRNA. /FEA=mRNA /GEN=PPP1R8 /PROD=protein phosphatase 1, regulatory (inhibitor) subunit 8 /DB_XREF=gi:4506014 /UG=Hs.78961 protein phosphatase 1, regulatory (inhibitor) subunit 8 /FL=gb:NM_002713.1 gb:U14575.1
204061_at	gb:NM_005044.1 /DEF=Homo sapiens protein kinase, X-linked (PRKX), mRNA. /FEA=mRNA /GEN=PRKX /PROD=protein kinase, X-linked /DB_XREF=gi:4826947 /UG=Hs.147996 protein kinase, X-linked /FL=gb:NM_005044.1

215633_x_at	Consensus includes gb:AV713720 /FEA=EST /DB_XREF=gi:10795237 /DB_XREF=est:AV713720 /CLONE=DCBBJA12 /UG=Hs.306434 Homo sapiens mRNA for LST-1N protein
208660_at	gb:BC000105.1 /DEF=Homo sapiens, similar to CG14740 gene product, clone MGC:2503, mRNA, complete cds. /FEA=mRNA /PROD=Similar to CG14740 gene product /DB_XREF=gi:12652712 /UG=Hs.239760 citrate synthase /FL=gb:BC000105.1 gb:AF047042.1 gb:NM 004077.1
218805_at	gb:NM 018384.1 /DEF=Homo sapiens hypothetical protein FLJ11296 (FLJ11296), mRNA. /FEA=mRNA /GEN=FLJ11296 /PROD=hypothetical protein FLJ11296 /DB_XREF=gi:8922984 /UG=Hs.26194 hypothetical protein FLJ11296 /FL=gb:NM 018384.1
217725_x_at	gb:NM 015640.1 /DEF=Homo sapiens PAI-1 mRNA-binding protein (PAI-RBP1), mRNA. /FEA=mRNA /GEN=PAI-RBP1 /PROD=PAI-1 mRNA-binding protein /DB_XREF=gi:7661625 /UG=Hs.165998 PAI-1 mRNA-binding protein /FL=gb:AL080119.1 gb:NM 015640.1
200802_at	gb:NM 006513.1 /DEF=Homo sapiens seryl-tRNA synthetase (SARS), mRNA. /FEA=mRNA /GEN=SARS /PROD=seryl-tRNA synthetase /DB_XREF=gi:5730028 /UG=Hs.4888 seryl-tRNA synthetase /FL=gb:BC000716.1 gb:NM 006513.1 gb:D49914.1
213203_at	Consensus includes gb:AI633709 /FEA=EST /DB_XREF=gi:4685039 /DB_XREF=est:th1f03.x1 /CLONE=IMAGE:2124125 /UG=Hs.30174 small nuclear RNA activating complex, polypeptide 5, 19kD
204640_s_at	gb:NM 003563.1 /DEF=Homo sapiens speckle-type POZ protein (SPOP), mRNA. /FEA=mRNA /GEN=SPOP /PROD=speckle-type POZ protein /DB_XREF=gi:4507182 /UG=Hs.129951 speckle-type POZ protein /FL=gb:BC003385.1 gb:NM 003563.1
202324_s_at	gb:NM 022735.1 /DEF=Homo sapiens golgi resident protein GCP60 (GCP60), mRNA. /FEA=mRNA /GEN=GCP60 /PROD=golgi resident protein GCP60 /DB_XREF=gi:12232390 /UG=Hs.6831 golgi resident protein GCP60 /FL=gb:AB043587.1 gb:NM 022735.1
211661_x_at	gb:M80436.1 /DEF=Human platelet activating factor receptor mRNA, complete cds. /FEA=mRNA /GEN=PTAFR /PROD=platelet activating factor receptor /DB_XREF=gi:189537 /FL=gb:M80436.1
208969_at	gb:AF050641.1 /DEF=Homo sapiens NADH-ubiquinone oxidoreductase 39kDa subunit mRNA, nuclear gene encoding mitochondrial protein, complete cds. /FEA=mRNA /PROD=NADH-ubiquinone oxidoreductase 39kDa subunit /DB_XREF=gi:5326822 /UG=Hs.75227 NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 9 (39kD) /FL=gb:AF050641.1 gb:NM 005002.1
202227_s_at	gb:NM 006696.1 /DEF=Homo sapiens thyroid hormone receptor coactivating protein (SMAP), mRNA. /FEA=mRNA /GEN=SMAP /PROD=thyroid hormone receptor coactivating protein /DB_XREF=gi:5730052 /UG=Hs.5464 thyroid hormone receptor coactivating protein /FL=gb:AF016270.1 gb:NM 006696.1
221989_at	Consensus includes gb:AW057781 /FEA=EST /DB_XREF=gi:5933420 /DB_XREF=est:wx03f09.x1 /CLONE=IMAGE:2542601 /UG=Hs.29797 ribosomal protein L10
202545_at	gb:NM 006254.1 /DEF=Homo sapiens protein kinase C, delta (PRKCD), mRNA. /FEA=mRNA /GEN=PRKCD /PROD=protein kinase C, delta /DB_XREF=gi:5453969 /UG=Hs.155342 protein kinase C, delta /FL=gb:U07860.1 gb:U07861.1 gb:D10495.1 gb:NM 006254.1
202214_s_at	gb:NM 003588.1 /DEF=Homo sapiens cullin 4B (CUL4B), mRNA. /FEA=mRNA /GEN=CUL4B /PROD=cullin 4B /DB_XREF=gi:13270466 /UG=Hs.155976 cullin 4B /FL=gb:NM 003588.1 gb:AB014595.1
218366_x_at	gb:NM 022734.1 /DEF=Homo sapiens hypothetical protein FLJ20859 (FLJ20859), mRNA. /FEA=mRNA /GEN=FLJ20859 /PROD=hypothetical protein FLJ20859 /DB_XREF=gi:12232388 /UG=Hs.6311 hypothetical protein FLJ20859 /FL=gb:NM 022734.1
218592_s_at	gb:NM 017829.1 /DEF=Homo sapiens hypothetical protein FLJ20454 (FLJ20454), mRNA. /FEA=mRNA /GEN=FLJ20454 /PROD=hypothetical protein FLJ20454 /DB_XREF=gi:8923424 /UG=Hs.26890 hypothetical protein FLJ20454 /FL=gb:AF273271.1 gb:NM 017829.1
209658_at	gb:AF164598.1 /DEF=Homo sapiens cell division control protein 16 (CDC16) mRNA, complete cds. /FEA=mRNA /GEN=CDC16 /PROD=cell division control protein 16 /DB_XREF=gi:5533374 /UG=Hs.1592 CDC16 (cell division cycle 16, S. cerevisiae, homolog) /FL=gb:AF164598.1
202217_at	gb:NM 004649.1 /DEF=Homo sapiens ESI (zebrafish) protein, human homolog of (C21ORF33), mRNA. /FEA=mRNA /GEN=C21ORF33 /PROD=ESI (zebrafish) protein, human homolog of /DB_XREF=gi:5031690 /UG=Hs.182423 ESI (zebrafish) protein, human homolog of /FL=gb:BC002370.1 gb:BC003587.1 gb:D86061.1 gb:U53003.1 gb:NM 004649.1
54970_at	Cluster Incl. AA868332:ak40H05.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1408473 /clone_end=3 /gb=AA868332 /gi=2963777 /ug=Hs.77978 /len=481

202441_at	Consensus includes gb:AL568449 /FEA=EST /DB_XREF=gi:12922799 /DB_XREF=est:AL568449 /CLONE=CS0DE001YC12 (3 prime) /UG=Hs.285818 similar to Caenorhabditis elegans protein C42C1.9 /FL=gb:AF064093.1 gb:NM 006459.1
211383_s_at	gb:AL136827.1 /DEF=Homo sapiens mRNA; cDNA DKFZp434F2427 (from clone DKFZp434F2427); complete cds. /FEA=mrna /GEN=DKFZp434F2427 /PROD=hypothetical protein /DB_XREF=gi:6807664 /UG=Hs.27207 KIAA0982 protein /FL=gb:AL136827.1
201903_at	gb:NM 003365.1 /DEF=Homo sapiens ubiquinol-cytochrome c reductase core protein I (UCRC1), mRNA. /FEA=mrna /GEN=UCRC1 /PROD=ubiquinol-cytochrome c reductase core protein I /DB_XREF=gi:4507840 /UG=Hs.119251 ubiquinol-cytochrome c reductase core protein I /FL=gb:L16842.1 gb:NM 003365.1 gb:D26485.1
201827_at	gb:AF113019.1 /DEF=Homo sapiens PRO2451 mRNA, complete cds. /FEA=mrna /PROD=PRO2451 /DB_XREF=gi:6642761 /UG=Hs.250581 SWISNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 2
201583_s_at	/FL=gb:U66618.1 gb:NM 003077.1 gb:AF113019.1
210825_s_at	gb:NM 006363.1 /DEF=Homo sapiens Sec23 (S. cerevisiae) homolog B (SEC23B), mRNA. /FEA=mrna /GEN=SEC23B /PROD=Sec23 (S. cerevisiae) homolog B /DB_XREF=gi:5454043 /UG=Hs.173497 Sec23 (S. cerevisiae) homolog B /FL=gb:BC005404.1 gb:NM 006363.1
212696_s_at	gb:AF130103.1 /DEF=Homo sapiens clone FLB2914 PRO0720 mRNA, complete cds. /FEA=mrna /PROD=PRO0720 /DB_XREF=gi:11493509 /UG=Hs.160483 erythrocyte membrane protein band 7.2 (stomatrin) /FL=gb:AF130103.1
218229_s_at	Consensus includes gb:BF968633 /FEA=EST /DB_XREF=gi:12335848 /DB_XREF=est:602271068F1 /CLONE=IMAGE:4359209 /UG=Hs.66394 ring finger protein 4
210111_s_at	gb:NM 017542.1 /DEF=Homo sapiens KIAA1513 protein (KIAA1513), mRNA. /FEA=mrna /GEN=KIAA1513 /PROD=KIAA1513 protein /DB_XREF=gi:8923835 /UG=Hs.284227 KIAA1513 protein /FL=gb:NM 017542.1
201268_at	gb:AF277175.1 /DEF=Homo sapiens PNAS-138 mRNA, complete cds. /FEA=mrna /PROD=PNAS-138 /DB_XREF=gi:12751080 /UG=Hs.326790 Homo sapiens PNAS-138 mRNA, complete cds /FL=gb:AF277175.1
201199_s_at	gb:NM 002512.1 /DEF=Homo sapiens non-metastatic cells 2, protein (NM23B) expressed in (NME2), nuclear gene encoding mitochondrial protein, mRNA. /FEA=mrna /GEN=NME2 /PROD=non-metastatic cells 2, protein (NM23B) expressed in /DB_XREF=gi:4505408 /UG=Hs.275163 non-metastatic cells 2, protein (NM23B) expressed in /FL=gb:BC002476.1 gb:M36981.1 gb:L16785.1 gb:NM 002512.1
218242_s_at	gb:NM 002807.1 /DEF=Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 1 (PSMD1), mRNA. /FEA=mrna /GEN=PSMD1 /PROD=proteasome (prosome, macropain) 26S subunit, non-ATPase, 1 /DB_XREF=gi:4506224 /UG=Hs.3887 proteasome (prosome, macropain) 26S subunit, non-ATPase, 1 /FL=gb:D44466.1 gb:NM 002807.1
201232_s_at	gb:NM 017635.1 /DEF=Homo sapiens hypothetical protein FLJ20039 (FLJ20039), mRNA. /FEA=mrna /GEN=FLJ20039 /PROD=hypothetical protein FLJ20039 /DB_XREF=gi:8923045 /UG=Hs.267448 hypothetical protein FLJ20039 /FL=gb:NM 017635.1
220044_x_at	gb:NM 002817.1 /DEF=Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 13 (PSMD13), mRNA. /FEA=mrna /GEN=PSMD13 /PROD=proteasome (prosome, macropain) 26S subunit, non-ATPase, 13 /DB_XREF=gi:4506222 /UG=Hs.279554 proteasome (prosome, macropain) 26S subunit, non-ATPase, 13 /FL=gb:BC001100.1 gb:BC001747.1 gb:AB009398.1
210835_s_at	gb:NM 002817.1 gb:AF083245.1 gb:AF107837.1
211271_x_at	gb:NM 016424.1 /DEF=Homo sapiens cisplatin resistance-associated overexpressed protein (LUC7A), mRNA. /FEA=mrna /GEN=LUC7A /PROD=cisplatin resistance-associated overexpressed protein /DB_XREF=gi:7706534 /UG=Hs.3688
218998_at	cisplatin resistance-associated overexpressed protein /FL=gb:NM 016424.1
201765_s_at	gb:AF222711.1 /DEF=Homo sapiens ribeye mRNA, complete cds. /FEA=mrna /PROD=ribeye /DB_XREF=gi:12034652 /UG=Hs.171391 C-terminal binding protein 2 /FL=gb:AF222711.1 gb:NM 022802.1
	gb:BC004383.1 /DEF=Homo sapiens, Similar to polypyrimidine tract binding protein (heterogeneous nuclear ribonucleoprotein I), clone MGC:10830, mRNA, complete cds. /FEA=mrna /PROD=Similar to polypyrimidine tract binding protein (heterogeneous nuclear ribonucleoprotein I) /DB_XREF=gi:13325139 /UG=Hs.172550 polypyrimidine tract binding protein (heterogeneous nuclear ribonucleoprotein I) /FL=gb:BC004383.1
	gb:NM 017832.1 /DEF=Homo sapiens hypothetical protein FLJ20457 (FLJ20457), mRNA. /FEA=mrna /GEN=FLJ20457 /PROD=hypothetical protein FLJ20457 /DB_XREF=gi:8923430 /UG=Hs.29276 hypothetical protein FLJ20457 /FL=gb:AF153417.1 gb:NM 017832.1
	Consensus includes gb:AL523158 /FEA=EST /DB_XREF=gi:12786651 /DB_XREF=est:ALS23158 /CLONE=CS0DC001YM06 (3 prime)

	/UG=Hs.119403 hexosaminidase A (alpha polypeptide) /FL=gb:NM_000520.2
204837_at	Consensus includes gb:AL080178.1 /DEF=Homo sapiens mRNA; cDNA DKFZp434K171 (from clone DKFZp434K171); partial cds. /FEA=mrna /GEN=DKFZp434K171 /PROD=hypothetical protein /DB_XREF=gi:5262652 /UG=Hs.27194 DKFZp434K171 protein /FL=gb:NM_015458.1
201221_s_at	gb:NM_003089.1 /DEF=Homo sapiens small nuclear ribonucleoprotein 70kD polypeptide (RNP antigen) (SNRP70), mRNA. /FEA=mrna /GEN=SNRP70 /PROD=small nuclear ribonucleoprotein 70kD polypeptide (RNP antigen) /DB_XREF=gi:4507118 /UG=Hs.174051 small nuclear ribonucleoprotein 70kD polypeptide (RNP antigen) /FL=gb:BC000342.1 gb:M22636.1 gb:NM_003089.1
209092_s_at	gb:AF061730.1 /DEF=Homo sapiens clone 016003 My027 protein mRNA, complete cds. /FEA=mrna /PROD=My027 protein /DB_XREF=gi:12001995 /UG=Hs.279061 CGI-150 protein /FL=gb:AF061730.1 gb:AF151908.1 gb:NM_016080.1
202265_at	gb:NM_005180.1 /DEF=Homo sapiens murine leukemia viral (bmi-1) oncogene homolog (Bmi1), mRNA. /FEA=mrna /GEN=Bmi1 /PROD=murine leukemia viral (bmi-1) oncogene homolog /DB_XREF=gi:4885094 /UG=Hs.431 murine leukemia viral (bmi-1) oncogene homolog /FL=gb:U13689.1 gb:NM_005180.1
203721_s_at	gb:NM_016001.1 /DEF=Homo sapiens CGI-48 protein (LOC51096), mRNA. /FEA=mrna /GEN=LOC51096 /PROD=CGI-48 protein /DB_XREF=gi:7705764 /UG=Hs.6153 CGI-48 protein /FL=gb:AF151806.1 gb:NM_016001.1
202475_at	gb:NM_006326.1 /DEF=Homo sapiens seven transmembrane domain protein (NIFIE14), mRNA. /FEA=mrna /GEN=NIFIE14 /PROD=seven transmembrane domain protein /DB_XREF=gi:5453781 /UG=Hs.9234 seven transmembrane domain protein /FL=gb:BC001118.1 gb:NM_006326.1
213165_at	Consensus includes gb:AI041204 /FEA=EST /DB_XREF=gi:3280398 /DB_XREF=est:ov77g06.xl /CLONE=IMAGE:1643386 /UG=Hs.323748 Homo sapiens clone CDAP0086 mRNA sequence
213198_at	Consensus includes gb:AL117643.1 /DEF=Homo sapiens mRNA; cDNA DKFZp434M245 (from clone DKFZp434M245). /FEA=mrna /DB_XREF=gi:5912233 /UG=Hs.5288 Homo sapiens mRNA; cDNA DKFZp434M245 (from clone DKFZp434M245)
212837_at	Consensus includes gb:D63877.1 /DEF=Human mRNA for KIAA0157 gene, partial cds. /FEA=mrna /GEN=KIAA0157 /DB_XREF=gi:961445 /UG=Hs.82324 KIAA0157 protein
206592_s_at	gb:NM_003938.1 /DEF=Homo sapiens adaptor-related protein complex 3, delta 1 subunit (AP3D1), mRNA. /FEA=mrna /GEN=AP3D1 /PROD=adaptor-related protein complex 3, delta 1 subunit /DB_XREF=gi:4501976 /UG=Hs.75056 adaptor-related protein complex 3, delta 1 subunit /FL=gb:U91930.1 gb:NM_003938.1
212694_s_at	Consensus includes gb:NM_000532.1 /DEF=Homo sapiens propionyl Coenzyme A carboxylase, beta polypeptide (PCCB), nuclear gene encoding mitochondrial protein, mRNA. /FEA=cds /GEN=PCCB /PROD=propionyl Coenzyme A carboxylase, beta polypeptide /DB_XREF=gi:4557043 /UG=Hs.63788 propionyl Coenzyme A carboxylase, beta polypeptide /FL=gb:NM_000532.1
211759_x_at	gb:BC005969.1 /DEF=Homo sapiens, clone MGC:14625, mRNA, complete cds. /FEA=mrna /PROD=Unknown (protein for MGC:14625) /DB_XREF=gi:13543641 /FL=gb:BC005969.1
212714_at	Consensus includes gb:AL050205.1 /DEF=Homo sapiens mRNA; cDNA DKFZp586F1323 (from clone DKFZp586F1323). /FEA=mrna /DB_XREF=gi:4884444 /UG=Hs.26613 Homo sapiens mRNA; cDNA DKFZp586F1323 (from clone DKFZp586F1323)
201528_at	Consensus includes gb:BG398414 /FEA=EST /DB_XREF=gi:13291862 /DB_XREF=est:602439888F1 /CLONE=IMAGE:4566380 /UG=Hs.84318 replication protein A1 (70kD) /FL=gb:M63488.1 gb:NM_002945.1
211795_s_at	gb:AF198052.1 /DEF=Homo sapiens EVH1 domain binding protein mRNA, complete cds. /FEA=cds /PROD=EVH1 domain binding protein /DB_XREF=gi:7416992 /UG=Hs.58435 EVH1 domain binding protein (EVB-120130) /FL=gb:AF198052.1
218633_x_at	gb:NM_018394.1 /DEF=Homo sapiens hypothetical protein FLJ11342 (FLJ11342), mRNA. /FEA=mrna /GEN=FLJ11342 /PROD=hypothetical protein FLJ11342 /DB_XREF=gi:8923000 /UG=Hs.266514 hypothetical protein FLJ11342 /FL=gb:NM_018394.1
200800_s_at	gb:NM_005345.3 /DEF=Homo sapiens heat shock 70kD protein 1A (HSPA1A), mRNA. /FEA=mrna /GEN=HSPA1A /PROD=heat shock 70kD protein 1A /DB_XREF=gi:5579469 /UG=Hs.8997 heat shock 70kD protein 1A /FL=gb:BC002453.1 gb:NM_005345.3
214719_at	Consensus includes gb:AK026720.1 /DEF=Homo sapiens cDNA: FLJ23067 f1s, clone LNG04993
213655_at	Consensus includes gb:AA502643 /FEA=EST /DB_XREF=gi:2237610 /DB_XREF=est:ne42g05.s1 /CLONE=IMAGE:900056 /UG=Hs.79474 tyrosine 3-monooxygenase tryptophan
212371_at	5-monooxygenase activation protein, epsilon polypeptide Consensus includes gb:AL049397.1 /DEF=Homo sapiens mRNA; cDNA DKFZp586C1019 (from clone DKFZp586C1019). /FEA=mrna /DB_XREF=gi:4500188 /UG=Hs.12314
210166_at	Homo sapiens mRNA; cDNA DKFZp586C1019 (from clone DKFZp586C1019) gb:AF051151.1 /DEF=Homo sapiens Tollinterleukin-1 receptor-like protein 3 (TIL3) mRNA, complete cds. /FEA=mrna /GEN=TIL3 /PROD=Tollinterleukin-1 receptor-like protein 3 /DB_XREF=gi:3132525 /UG=Hs.114408 toll-like receptor 5 /FL=gb:AF051151.1
217958_at	gb:NM_016146.1 /DEF=Homo sapiens PTD009 protein (PTD009), mRNA. /FEA=mrna /GEN=PTD009 /PROD=PTD009 protein /DB_XREF=gi:7706666 /UG=Hs.279901 PTD009

219269_at	UG-Hs.279901 PTD009 protein /FL-gb:AF151862.1 gb:AF161520.1 gb:NM 016146.1
219574_at	gb:NM_024567.1 /DEF=Homo sapiens hypothetical protein FLJ21616 (FLJ21616), mRNA. /FEA=mrna /GEN=FLJ21616 /PROD=hypothetical protein FLJ21616 /DB XREF=gi:13375737 /UG=Hs.14562 hypothetical protein FLJ21616 /FL-gb:NM 024567.1
210183_x_at	gb:NM_017923.1 /DEF=Homo sapiens hypothetical protein FLJ20668 (FLJ20668), mRNA. /FEA=mrna /GEN=FLJ20668 /PROD=hypothetical protein FLJ20668 /DB XREF=gi:18923612 /UG=Hs.12920 hypothetical protein FLJ20668 /FL-gb:NM 017923.1
211582_x_at	gb:AF112222.1 /DEF=Homo sapiens nuclear protein SDK3 mRNA, complete cds. /FEA=mrna /PROD=nuclear protein SDK3 /DB XREF=gi:6563229 /UG=Hs.44499 pinin, desmosome associated protein /FL-gb:AF112222.1
212557_at	gb:AF000424.1 /DEF=Homo sapiens IST1 mRNA, cLSTIC splice variant, complete cds. /FEA=mrna /GEN=IST1 /DB XREF=gi:2145063 /UG=Hs.88411 Lymphocyte antigen 117 /FL-gb:AF000424.1
213387_at	Consensus includes gb:AB011148.1 /DEF=Homo sapiens mRNA for KIAA0576 protein, partial cds. /FEA=mrna /GEN=KIAA0576 protein /DB XREF=gi:3043675 /UG=Hs.172329 KIAA0576 protein
218143_s_at	Consensus includes gb:AB033066.1 /DEF=Homo sapiens mRNA for KIAA1240 protein, partial cds. /FEA=mrna /GEN=KIAA1240 protein /DB XREF=gi:6330790 /UG=Hs.82576 KIAA1240 protein
211615_s_at	gb:NM_005697.2 /DEF=Homo sapiens secretory carrier membrane protein 2 (SCAMP2), mRNA. /FEA=mrna /GEN=SCAMP2 /PROD=secretory carrier membrane protein 2 /DB XREF=gi:5730030 /UG=Hs.238030 secretory carrier membrane protein 2 /FL-gb:BC001376.1 gb:BC004385.1 gb:AF005038.2
213359_at	gb:NM_005697.2
217842_at	gb:N92439.1 /DEF=Human leucine-rich protein mRNA, complete cds. /FEA=mrna /PROD=leucine-rich protein; leucine-rich protein /DB XREF=gi:1177109 /FL-gb:N92439.1
207170_s_at	Consensus includes gb:W74620 /FEA=EST /DB XREF=gi:1384833 /DB XREF=est:zd77e04.s1 /CLONE=IMAGE:346686 /UG=Hs.303627 heterogeneous nuclear ribonucleoprotein D [AU-rich element RNA-binding protein 1, 37kD]
214352_s_at	gb:NM_016019.1 /DEF=Homo sapiens CGI-74 protein (LOC51631), mRNA. /FEA=mrna /GEN=LOC51631 /PROD=CGI-74 protein /DB XREF=gi:7706309 /UG=Hs.7194 CGI-74 protein /FL-gb:AF151832.1 gb:NM 016019.1
218287_s_at	gb:NM_015416.1 /DEF=Homo sapiens DKFZP586A011 protein (DKFZP586A011), mRNA. /FEA=mrna /GEN=DKFZP586A011 /PROD=DKFZP586A011 protein /DB XREF=gi:7661659 /UG=Hs.75984 DKFZP586A011 protein /FL-gb:NM 015416.1
204661_at	Consensus includes gb:BF673699 /FEA=EST /DB XREF=gi:11947594 /DB XREF=est:602136427F1 /CLONE=IMAGE:4272774 /UG=Hs.184050 v-Ki-ras2 Kirsten rat sarcoma 2 viral oncogene homolog
205545_x_at	gb:NM_012199.1 /DEF=Homo sapiens eukaryotic translation initiation factor 2C, 1 (EIF2C1), mRNA. /FEA=mrna /GEN=EIF2C1 /PROD=eukaryotic translation initiation factor 2C, 1 /DB XREF=gi:6912351 /UG=Hs.14520 eukaryotic translation initiation factor 2C, 1 /FL-gb:AF093097.1
213750_at	gb:NM_012199.1
221970_s_at	gb:NM_001803.1 /DEF=Homo sapiens CDW52 antigen (CAMPATH-1 antigen) (CDW52), mRNA. /FEA=mrna /GEN=CDW52 /PROD=CDW52 antigen (CAMPATH-1 antigen) /DB XREF=gi:4502760 /UG=Hs.276770 CDW52 antigen (CAMPATH-1 antigen) /FL-gb:BC000644.1 gb:NM 001803.1
218684_at	gb:NM_014280.1 /DEF=Homo sapiens splicing factor similar to dnaJ (SPF31), mRNA. /FEA=mrna /GEN=SPF31 /PROD=splicing factor similar to dnaJ /DB XREF=gi:7657610 /UG=Hs.74711 DnaJ (Hsp40) homolog, subfamily C, member 8 /FL-gb:AF083190.1 gb:NM 014280.1
200628_s_at	Consensus includes gb:AA928506 /FEA=EST /DB XREF=gi:3076797 /DB XREF=est:om17q03.s1 /CLONE=IMAGE:1541332 /UG=Hs.10762 ESTs
203905_at	Consensus includes gb:AUI58148 /FEA=EST /DB XREF=gi:11019669 /DB XREF=est:AUI58148 /CLONE=PLACE1011221 /UG=Hs.321105 Homo sapiens cDNA: FLJ21737 fis, clone COLF3396
204039_at	gb:NM_018103.1 /DEF=Homo sapiens hypothetical protein FLJ10470 (FLJ10470), mRNA. /FEA=mrna /GEN=FLJ10470 /PROD=hypothetical protein FLJ10470 /DB XREF=gi:8922441 /UG=Hs.41672 hypothetical protein FLJ10470 /FL-gb:NM 018103.1
63009_at	gb:M61715.1 /DEF=Human tryptophanyl-tRNA synthetase (WRS) mRNA, complete cds. /FEA=mrna /GEN=WARS /PROD=transfer RNA-Trp synthetase /DB XREF=gi:340367 /UG=Hs.82030 tryptophanyl-tRNA synthetase /FL-gb:MT7804.1 gb:M61715.1 gb:NM 004184.2
211922_s_at	gb:NM_002582.1 /DEF=Homo sapiens poly(A)-specific ribonuclease (deadenylation nuclease) (PARN), mRNA. /FEA=mrna /GEN=PARN /PROD=poly(A)-specific ribonuclease (deadenylation nuclease) /DB XREF=gi:4505610 /UG=Hs.43445 poly(A)-specific ribonuclease (deadenylation nuclease) /FL-gb:NM 002582.1
212861_at	gb:NM_004364.1 /DEF=Homo sapiens CCAATenhancer binding protein (CEBP), alpha (CEBPA), mRNA. /FEA=mrna /GEN=CEBPA /PROD=CCAATenhancer binding protein (CEBP), alpha /DB XREF=gi:4757971 /UG=Hs.76171 CCAATenhancer binding protein (CEBP), alpha /FL-gb:NM 004364.1
	Cluster Incl. A1188402:qd08e03.x1 Homo sapiens cDNA, 3' end /clone=IMAGE-1723132 /clone_end=3 /gb=A1188402 /gi=3739611 /ug=Hs.93391 /len=506
	gb:AY028632.1 /DEF=Homo sapiens catalase (CAT) mRNA, complete cds. /FEA=cds /GEN=CAT /PROD=catalase /DB XREF=gi:13562131 /FL-gb:AY028632.1
	Consensus includes gb:BF690150 /FEA=EST /DB XREF=gi:11975558 /DB XREF=est:602186478T1 /CLONE=IMAGE:4298635 /UG=Hs.19210 ESTs

206715_at	gb:NM_012252.1 / DEF=Homo sapiens transcription factor EC (TFEC), mRNA. / FEA=mrna / GEN=KIAA0680 / PROD=transcription factor EC
213123_at	Consensus includes gb:BE222709 / FEA=EST / DB_XREF=gi:8910027 / DB_XREF=est:hu51q06.x1 / CLONE=IMAGE:3173626 / UG=Hs.28785 microfibrillar-associated protein 3
204049_s_at	gb:NM_014721.1 / DEF=Homo sapiens KIAA0680 gene product (KIAA0680), mRNA. / FEA=mrna / GEN=KIAA0680 / PROD=KIAA0680 gene product
201985_at	gb:NM_014846.1 / DEF=Homo sapiens KIAA0196 gene product (KIAA0196), mRNA. / FEA=mrna / GEN=KIAA0196 / PROD=KIAA0196 gene product
208773_s_at	gb:NM_014846.1 / DEF=Homo sapiens KIAA0196 gene product (KIAA0196), mRNA. / FEA=mrna / GEN=KIAA0196 / PROD=KIAA0196 gene product
219563_at	gb:NM_014846.1 / DEF=Homo sapiens KIAA0196 gene product (KIAA0196), mRNA. / FEA=mrna / GEN=KIAA0196 / PROD=KIAA0196 gene product
218501_at	gb:NM_014846.1 / DEF=Homo sapiens KIAA0196 gene product (KIAA0196), mRNA. / FEA=mrna / GEN=KIAA0196 / PROD=KIAA0196 gene product
212833_at	Consensus includes gb:M74089.1 / DEF=Human TBI gene mRNA, 3 end. / FEA=mrna / GEN=TBI / DB_XREF=gi:182400 / UG=Hs.75639 Human TBI gene mRNA, 3 end
209623_at	Consensus includes gb:AW439494 / FEA=EST / DB_XREF=gi:6974800 / DB_XREF=est:xt19c01.x1 / CLONE=IMAGE:2779584 / UG=Hs.167531 methylcrotonoyl-Coenzyme A carboxylase 2 (beta) / FL=gb:AB050049.1 gb:AF310971.1 gb:AF301000.1 gb:NM_022132.2
209969_s_at	gb:BC002704.1 / DEF=Homo sapiens, Similar to signal transducer and activator of transcription 1, 91kd, clone MGC:3493, mRNA, complete cds. / FEA=mrna / PROD=Similar to signal transducer and activator of transcription 1, 91kd / DB_XREF=gi:12803734 / UG=Hs.21486 signal transducer and activator of transcription 1, 91kd / FL=gb:BC002704.1
219966_x_at	gb:NM_017869.1 / DEF=Homo sapiens BANP homolog, SMAR1 homolog (FLJ20538), mRNA. / FEA=mrna / GEN=FLJ20538 / PROD=BANP homolog, SMAR1 homolog / DB_XREF=gi:8923506 / UG=Hs.194637 BANP homolog, SMAR1 homolog / FL=gb:NM_017869.1
213275_x_at	Consensus includes gb:W47179 / FEA=EST / DB_XREF=gi:1332046 / DB_XREF=est:zc34d07.s1 / CLONE=IMAGE:324205 / UG=Hs.297939 cathepsin B
210231_x_at	gb:BC001669.1 / DEF=Homo sapiens, Similar to template acylating factor-I alpha, complete cds. / FEA=mrna / GEN=set / PROD=template acylating factor-I alpha / DB_XREF=gi:971271 / UG=Hs.145279 SET translocation (myeloid leukemia-associated) / FL=gb:BC001669.1
212474_at	Consensus includes gb:D87682.1 / DEF=Human mRNA for KIAA0241 gene, partial cds. / FEA=mrna / GEN=KIAA0241 / DB_XREF=gi:1663699 / UG=Hs.150275 KIAA0241 protein
208717_at	gb:BC001669.1 / DEF=Homo sapiens, Similar to oxidase (cytochrome c) assembly 1-like, clone MGC:2171, mRNA, complete cds. / FEA=mrna / PROD=Similar to oxidase (cytochrome c) assembly 1-like / DB_XREF=gi:12804516 / UG=Hs.151134 oxidase (cytochrome c) assembly 1-like / FL=gb:BC001669.1
217527_s_at	Consensus includes gb:AL478300 / FEA=EST / DB_XREF=gi:4371526 / DB_XREF=est:tm39e01.x1 / CLONE=IMAGE:2160504 / UG=Hs.192789 ESTs, Weakly similar to ALU6 HUMAN ALU SUBFAMILY SP SEQUENCE CONTAMINATION WARNING ENTRY H.sapiens
220495_s_at	gb:NM_024715.1 / DEF=Homo sapiens hypothetical protein FLJ22625, mRNA. / FEA=mrna / GEN=FLJ22625 / PROD=hypothetical protein FLJ22625 / DB_XREF=gi:13376016 / UG=Hs.106534 hypothetical protein FLJ22625 / FL=gb:NM_024715.1
200892_s_at	gb:BC000451.1 / DEF=Homo sapiens, splicing factor, arginineserine-rich (transformer 2 Drosophila homolog) 10, clone MGC:8454, mRNA, complete cds. / FEA=mrna / PROD=splicing factor, arginineserine-rich (transformer 2 Drosophila homolog) 10 / DB_XREF=gi:12653362 / UG=Hs.30035 splicing factor, arginineserine-rich (transformer 2 Drosophila homolog) 10 / FL=gb:BC000451.1 gb:BC000451.1 gb:U61267.1 gb:U68063.1 gb:NM_004593.1
201798_s_at	gb:NM_013451.1 / DEF=Homo sapiens fer-1 (C.elegans)-like 3 (myoferlin) (FER1L3), mRNA. / FEA=mrna / GEN=FER1L3 / PROD=fer-1 (C.elegans)-like 3 (myoferlin) / DB_XREF=gi:7305052 / UG=Hs.234680 fer-1 (C.elegans)-like 3 (myoferlin) / FL=gb:AF182316.1 gb:NM_013451.1
202529_at	gb:NM_002766.1 / DEF=Homo sapiens phosphoribosyl pyrophosphate synthetase-associated protein 1 (PPRSAP1), mRNA. / FEA=mrna / GEN=PPRSAP1 / PROD=phosphoribosyl pyrophosphate synthetase-associated protein 1 / DB_XREF=gi:4506130 / UG=Hs.77498 phosphoribosyl pyrophosphate synthetase-associated protein 1 / FL=gb:U61391.1 gb:NM_002766.1
208897_s_at	gb:BC003360.1 / DEF=Homo sapiens, DEAD (Asp-Glu-Ala-AspHis) box polypeptide 18 (Myc-regulated), clone MGC:5316, mRNA, complete cds. / FEA=mrna / PROD=DEAD (Asp-Glu-Ala-AspHis) box polypeptide 18 (Myc-regulated) / DB_XREF=gi:13097182 / UG=Hs.100555 DEADH (Asp-Glu-Ala-AspHis) box polypeptide 18 (Myc-regulated) / FL=gb:BC003360.1
210296_s_at	gb:BC005375.1 / DEF=Homo sapiens, peroxisomal membrane protein 3 (35kd, Zellweger syndrome), clone MGC:12491, mRNA, complete cds. / FEA=mrna / PROD=peroxisomal membrane protein 3 (35kd, Zellweger syndrome) / DB_XREF=gi:13529226 / UG=Hs.180612 peroxisomal membrane protein 3 (35kd, Zellweger syndrome) / FL=gb:BC005375.1
212460_at	Consensus includes gb:BE738425 / FEA=EST / DB_XREF=gi:10152417 / DB_XREF=est:601572441T1 / CLONE=IMAGE:3839147 / UG=Hs.241507 ribosomal protein S6

211800_s_at	gb:AF017306.1 /DEF=Homo sapiens deubiquitinating enzyme UnpES (UNP) mRNA, complete cds. /FEA=CDS /GEN=UNP /PROD=UnpES /DB_XREF=gi:2656142 /UG=Hs.77500 ubiquitin specific protease 4 (proto-oncogene) /FL=gb:AF017306.1
202850_at	gb:NM_002858.2 /DEF=Homo sapiens ATP-binding cassette, sub-family D (ALD), member 3 (ABCD3), mRNA. /FEA=mrna /GEN=ABCD3 /PROD=ATP-binding cassette, sub-family D, member 3 /DB_XREF=gi:10947125 /UG=Hs.76781 ATP-binding cassette, sub-family D (ALD), member 3 /FL=gb:NM_002858.2 /gb:M81182.1
212202_s_at	Consensus includes gb:BG493972 /FEA=EST /DB_XREF=gi:13455486 /DB_XREF=est:602542252FT /CLONE=IMAGE:4673316 /UG=Hs.16492 DKFZP564G2022 protein
209337_at	gb:AF063020.1 /DEF=Homo sapiens lens epithelium-derived growth factor mRNA, complete cds. /FEA=mrna /PROD=lens epithelium-derived growth factor /DB_XREF=gi:3283351 /UG=Hs.82110 PC4 and SFRS1 interacting protein 1 /FL=gb:NM_021144.1 /gb:AF063020.1
207616_s_at	gb:NM_004180.1 /DEF=Homo sapiens TRAF family member-associated NFKB activator (TANK), mRNA. /FEA=mrna /GEN=TANK /PROD=TRAF family member-associated NFKB activator /DB_XREF=gi:4759249 /UG=Hs.14684 TRAF family member-associated NFKB activator /FL=gb:U63830.1 /gb:NM_004180.1
204630_s_at	gb:NM_004871.1 /DEF=Homo sapiens golgi SNAP receptor complex member 1 (GOSR1), mRNA. /FEA=mrna /GEN=GOSR1 /PROD=golgi SNAP receptor complex member 1 /DB_XREF=gi:4758455 /UG=Hs.8868 golgi SNAP receptor complex member 1 /FL=gb:AF073926.1 /gb:NM_004871.1
209422_at	Consensus includes gb:AL109965 /DEF=Human DNA sequence from clone RP5-1121G12 on chromosome 20 contains the 3' end of a gene encoding two isoforms (the hepatocellular carcinoma-associated antigen 58 (HCA58) and a putative novel protein containing a PHD finger domain), the SCAND1 gene... /FEA=mrna 2 /DB_XREF=gi:9663113 /UG=Hs.112594 hypothetical protein DKFZp344F0272 /FL=gb:AY027523.1 /gb:AF348207.1
203658_at	gb:BC001689.1 /DEF=Homo sapiens, carnitineacylcarnitine translocase, clone MGC:1207, mRNA, complete cds. /FEA=mrna /PROD=carnitineacylcarnitine translocase /DB_XREF=gi:12804552 /UG=Hs.13845 solute carrier family 25 (carnitineacylcarnitine translocase), member 20 /FL=gb:BC001689.1 /gb:NM_000387.2
212015_x_at	Consensus includes gb:BF690062 /FEA=EST /DB_XREF=gi:11975470 /DB_XREF=est:602186366T1 /CLONE=IMAGE:4298440 /UG=Hs.172550 polypyrimidine tract binding protein (heterogeneous nuclear ribonucleoprotein 1)
222122_s_at	Consensus includes gb:BG403671 /FEA=EST /DB_XREF=gi:13297119 /DB_XREF=est:602419393F1 /CLONE=IMAGE:4526326 /UG=Hs.16411 hypothetical protein LOC571187
202171_at	Consensus includes gb:AU146275 /FEA=EST /DB_XREF=gi:11007796 /DB_XREF=est:AU146275 /CLONE=HEM8B1000004 /UG=Hs.6557 zinc finger protein 161 /FL=gb:D28118.1 /gb:NM_007146.1
210460_s_at	gb:AB033605.1 /DEF=Homo sapiens mRNA for PUB-R5, complete cds. /FEA=mrna /GEN=hpUB-R5 /PROD=pub-R5 /DB_XREF=gi:8918352 /UG=Hs.148495 proteasome (prosome, macropain) 26S subunit, non-ATPase, 4 /FL=gb:AB033605.1
207551_s_at	gb:NM_006800.1 /DEF=Homo sapiens male-specific lethal-3 (Drosophila)-like 1 (MSL3L1), mRNA. /FEA=mrna /GEN=MSL3L1 /PROD=male-specific lethal-3 (Drosophila)-like 1 /DB_XREF=gi:5803103 /UG=Hs.88764 male-specific lethal-3 (Drosophila)-like 1 /FL=gb:AF117065.1 /gb:NM_006800.1
201104_x_at	gb:NM_015383.1 /DEF=Homo sapiens hypothetical protein (DJ328E19.C1.1), mRNA. /FEA=mrna /GEN=DJ328E19.C1.1 /PROD=hypothetical protein /DB_XREF=gi:7657016 /UG=Hs.218329 hypothetical protein /FL=gb:NM_015383.1
200812_at	gb:NM_006429.1 /DEF=Homo sapiens chaperonin containing TCPI, subunit 7 (eta) (CCT7), mRNA. /FEA=mrna /GEN=CCT7 /PROD=chaperonin containing TCPI, subunit 7 (eta) /DB_XREF=gi:5453606 /UG=Hs.108809 chaperonin containing TCPI, subunit 7 (eta) /FL=gb:AF026292.1 /gb:NM_006429.1
203494_s_at	gb:NM_014679.1 /DEF=Homo sapiens KIAA0092 gene product (KIAA0092), mRNA. /FEA=mrna /GEN=KIAA0092 /PROD=KIAA0092 gene product /DB_XREF=gi:7661899 /UG=Hs.151791 KIAA0092 gene product /FL=gb:D42054.1 /gb:NM_014679.1
202127_at	Consensus includes gb:AB011108.1 /DEF=Homo sapiens mRNA for KIAA0536 protein, partial cds. /FEA=mrna /GEN=KIAA0536 /PROD=KIAA0536 protein /DB_XREF=gi:3043595 /UG=Hs.198891 serine/threonine-protein kinase PRP4 homolog /FL=gb:U48736.1 /gb:NM_003913.1
212532_s_at	Consensus includes gb:AW873564 /FEA=EST /DB_XREF=gi:8007617 /DB_XREF=est:ho62c10.x1 /CLONE=IMAGE:3041970 /UG=Hs.155485 huntingtin interacting protein 2
218357_s_at	gb:NM_012459.1 /DEF=Homo sapiens translocase of inner mitochondrial membrane 8 (yeast) homolog B (TIMM8B), mRNA. /FEA=mrna /GEN=TIMM8B /PROD=translocase of inner mitochondrial membrane 8 (yeast) homolog B /DB_XREF=gi:6912711 /UG=Hs.279915 translocase of inner mitochondrial membrane 8 (yeast) homolog B /FL=gb:AF152350.1 /gb:NM_012459.1
208847_s_at	gb:M29872.1 /DEF=Human alcohol dehydrogenase class III (ADH5), complete cds. /FEA=mrna /GEN=ADH5 /DB_XREF=gi:178131 /UG=Hs.78989 alcohol dehydrogenase 5 (class III), chi polypeptide /FL=gb:NM_000671.2 /gb:M29872.1 /gb:M30471.1
207730_x_at	gb:NM_017932.1 /DEF=Homo sapiens hypothetical protein FLJ20700 (ELJ20700), mRNA. /FEA=mrna /GEN=FLJ20700 /PROD=hypothetical protein FLJ20700 /DB_XREF=gi:8923629 /UG=Hs.272222 hypothetical protein FLJ20700 /FL=gb:NM_017932.1
212896_at	Consensus includes gb:D29641.2 /DEF=Homo sapiens mRNA for KIAA0052 protein, partial cds. /FEA=mrna /GEN=KIAA0052 /PROD=KIAA0052 protein /DB_XREF=gi:6633994 /UG=Hs.278608 KIAA0052 protein
203156_at	gb:NM_016248.1 /DEF=Homo sapiens A-kinase anchoring protein 220 (LOCS1707), mRNA. /FEA=mrna /GEN=LOCS1707 /PROD=A-kinase anchoring protein 220 /DB_XREF=gi:7706455 /UG=Hs.232076 A kinase (PRKA) anchor protein 11 /FL=gb:AF176555.1 /gb:NM_016248.1
220066_at	gb:NM_022162.1 /DEF=Homo sapiens NOD2 protein (NOD2), mRNA. /FEA=mrna /GEN=NOD2 /PROD=NOD2 protein /DB_XREF=gi:11545911 /UG=Hs.135201 NOD2 protein /FL=gb:AF178930.1 /gb:NM_022162.1

	protein /FL-gb:AF178930.1 gb:NM_022162.1	
218583_s_at	gb:NM_020640.1 /DEF=Homo sapiens RP42 homolog (RP42), mRNA. /FEA-mRNA /GEN=RP42 /PROD=RP42 homolog /DB_XREF=gi:10190677 /UG-Hs.104613 RP42 homolog /FL-gb:NM_020640.1 gb:AF292100.2	
221689_s_at	gb:AB035745.1 /DEF=Homo sapiens mRNA for DSCR5b, complete cds. /FEA-mRNA /GEN=DSCR5b /PROD=DSCR5b /DB_XREF=gi:7798596 /UG-Hs.66493 Down syndrome critical region gene 5 /FL-gb:AB035745.1 gb:AB037163.1 gb:AF237812.1	
205412_at	gb:NM_000019.1 /DEF=Homo sapiens acetyl-Coenzyme A acetyltransferase 1 (acetoacetyl Coenzyme A thiolase) (ACATL1), nuclear gene encoding mitochondrial protein, mRNA. /FEA-mRNA /GEN=ACATL1 /PROD=acetyl-Coenzyme A acetyltransferase 1 (acetoacetyl Coenzyme A thiolase) /FL-gb:NM_000019.1	
202542_s_at	gb:NM_004757.1 /DEF=Homo sapiens small inducible cytokine subfamily E, member 1 (endothelial monocyte-activating factor 1 alpha) /DB_XREF=gi:4758265 /UG-Hs.146401 small inducible cytokine subfamily E, member 1 (endothelial monocyte-activating) /FL-gb:NM_004757.1 gb:U01017.1	
202521_at	gb:NM_006565.1 /DEF=Homo sapiens CCCTC-binding factor (zinc finger protein) (CTCF), mRNA. /FEA-mRNA /GEN=CTCF /PROD=CCCTC-binding factor (zinc finger protein) /DB_XREF=gi:5729789 /UG-Hs.57419 CCCTC-binding factor (zinc finger protein) /FL-gb:NM_006565.1 gb:U25435.1	
204391_x_at	gb:NM_015905.1 /DEF=Homo sapiens transcriptional intermediary factor 1 (TIF1), mRNA. /FEA-mRNA /GEN=TIF1 /PROD-transcriptional intermediary factor 1 alpha /DB_XREF=gi:7706233 /UG-Hs.183858 transcriptional intermediary factor 1 /FL-gb:AF009353.1 gb:AF119042.1 gb:NM_003852.1	
214733_s_at	Consensus includes gb:AU031427 /DEF=Human DNA sequence from clone l67A19 on chromosome lp32.1-33. Contains three genes for novel proteins, the DT01 gene for type I iodothyronine deiodinase (SC 3.8.1.i.4, TXD11, ITD11) and an HNRNP A3 (Heterogenous Nuclear Ribonucleoprotein A3, FBRNP) ... /FEA-mRNA 6 /DB_XREF=gi:4835258 /UG-Hs.11923 hypothetical protein	
2127864_s_at	gb:NM_016166.1 /DEF=Homo sapiens DEADH (Asp-Glu-Ala-AspHis) box binding protein 1 (DDXBPL1), mRNA. /FEA-mRNA /GEN=DDXBPL1 /PROD=DEADH (Asp-Glu-Ala-AspHis) box binding protein1 /DB_XREF=gi:7706636 /UG-Hs.75251 DEADH (Asp-Glu-Ala-AspHis) box binding protein 1 /FL-gb:AF167160.1 gb:NM_016166.1	
212904_at	Consensus includes gb:AB033011.1 /DEF=Homo sapiens mRNA for KIAA1185 protein, partial cds. /FEA-mRNA /GEN=KIAA1185 /PROD=KIAA1185 protein /DB_XREF=gi:630301 /UG-Hs.268488 KIAA1185 protein	
20202126_at	Consensus includes gb:AA156948 /FEA=EST /DB_XREF=est:z119f02.s1 /CLONE=IMAGE:502395 /UG-Hs.198891 serinethreonine-protein kinase PRP4 homolog /FL-gb:U48736.1 gb:NM_003913.1	
20203484_at	gb:NM_014302.1 /DEF=Homo sapiens Sec61 gamma (SEC61G), mRNA. /FEA-mRNA /GEN=SEC61G /PROD=Sec61 gamma /DB_XREF=gi:7657545 /UG-Hs.9950 Sec61 gamma /FL-gb:AF054184.1 gb:NM_014302.1	
203345_s_at	Consensus includes gb:A1566096 /FEA=EST /DB_XREF=gi:4524548 /DB_XREF=est:n53402.x1 /CLONE=IMAGE:2112099 /UG-Hs.31016 putative DNA binding protein /FL-gb:AF072814.1 gb:NM_007358.1	
21213238_at	Consensus includes gb:A1478147 /FEA=EST /DB_XREF=est:tm34F06.x1 /CLONE=IMAGE:2160035 /UG-Hs.173540 ATPase, Class V, type 10D	
2020680_at	gb:NM_002095.1 /DEF=Homo sapiens general transcription factor IIE, polypeptide 2 (beta subunit, 34kd) (GT2E2), mRNA. /FEA-mRNA /GEN=GT2E2 /PROD-general transcription factor IIE, polypeptide 2(beta subunit, 34kd) /DB_XREF=gi:4504194 /UG-Hs.77100 general transcription factor IIE,	
21218117_at	polypeptide 2 (beta subunit, 34kd) /FL-gb:NM_002095.1	
21218117_at	gb:NM_014248.1 /DEF=Homo sapiens ring-box 1 (RBX1), mRNA. /FEA-mRNA /GEN=RBX1 /PROD=ring-box 1 /DB_XREF=gi:7657507 /UG-Hs.279919 ring-box 1 /FL-gb:BC001466.1 gb:AF140598.1 gb:AF142059.1 gb:NM_014248.1	
21218768_at	gb:NM_020401.1 /DEF=Homo sapiens nuclear pore complex protein (NUP107), mRNA. /FEA-mRNA /GEN=NUP107 /PROD=nuclear pore complex protein /DB_XREF=gi:9966880 /UG-Hs.236204 nuclear pore complex protein /FL-gb:NM_020401.1	
2022271_at	Consensus includes gb:AB007952.1 /DEF=Homo sapiens mRNA for KIAA0483 protein, partial cds. /FEA-mRNA /GEN=KIAA0483 /PROD=KIAA0483 protein /DB_XREF=gi:3413925 /UG-Hs.64691 KIAA0483 protein /FL-gb:NM_015176.1	
2021218543_s_at	gb:NM_022750.1 /DEF=Homo sapiens hypothetical protein FLJ22693 (FLJ22693), mRNA. /FEA-mRNA /GEN=FLJ22693 /PROD=hypothetical protein FLJ22693 /DB_XREF=gi:12232412 /UG-Hs.12646 hypothetical protein FLJ22693 /FL-gb:AL136766.1 gb:NM_022750.1	
20203146_s_at	gb:NM_001470.1 /DEF=Homo sapiens gamma-aminobutyric acid (GABA) B receptor, 1 (GABBR1), transcript variant 1, mRNA. /FEA-mRNA /GEN=GABBR1 /PROD=gamma-aminobutyric acid (GABA) B receptor 1, isoform precursor /DB_XREF=gi:10835014 /UG-Hs.167017 gamma-aminobutyric acid (GABA) B receptor, 1 /FL-gb:NM_001470.1 gb:AF301005.1 gb:AF099148.1	
21218140_x_at	gb:NM_021203.1 /DEF=Homo sapiens APWCF1 protein (APWCF1), mRNA. /FEA-mRNA /GEN=APWCF1 /PROD=APWCF1 protein /DB_XREF=gi:10864014 /UG-Hs.12152 APWCF1 protein /FL-gb:NM_021203.1 gb:AF141882.1	
204420_at	Cluster Incl. AB015718:Homo sapiens lok mRNA for protein kinase, complete cds /cds=(50,2956) /gb=AB015718 /gi=4001687 /ug=Hs.16134 /lens=4221	

209971_x_at	Consensus includes gb:AI928526 /FEA-EST /DB_XREF=gi:5664490 /DB_XREF=est:wp59a06.x1 /CLONE=IMAGE:2466034 /UG=Hs.258730 heme-regulated initiation factor 2-alpha kinase /FL=gb:AF116615.1
48580_at	Cluster Incl. U55777:HSU55777 Homo sapiens cDNA /clone=37698 /gb=U55777 /gi=1354513 /ug=Hs.180933 /len=1593
202416_at	gb:NM 003315.1 /DEF=Homo sapiens tetratricopeptide repeat domain 2 (TTC2), mRNA. /FEA-mRNA /GEN=FTC2 /PROD=tetratricopeptide repeat domain 2 /DB_XREF=gi:4507712 /UG=Hs.5542 DnaJ (Hsp40) homolog, subfamily C, member 7 /FL=gb:U46571.1 gb:NM 003315.1
211727_s_at	gb:BC005895.1 /DEF=Homo sapiens, COX11 (yeast) homolog, cytochrome c oxidase assembly protein /DB_XREF=gi:13543474 /FL=gb:BC005895.1 /FEA-mRNA /PROD=COX11 (yeast) homolog, cytochrome c oxidase assembly protein
202125_s_at	gb:NM 015049.1 /DEF=Homo sapiens amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 3 (ALS2CR3), mRNA. /FEA-mRNA /GEN=ALS2CR3 /PROD=amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 3 /DB_XREF=gi:13027379 /UG=Hs.154248 amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 3 /FL=gb:AB038951.1 gb:NM 015049.1
209451_at	gb:U59863.1 /DEF=Human TRAF-interacting protein I-TRAF mRNA, complete cds. /FEA-mRNA /PROD=I-TRAF /DB_XREF=gi:1518017 /UG=Hs.146847 TRAF family member-associated NFKB activator /FL=gb:U59863.1
209440_at	gb:BC001605.1 /DEF=Homo sapiens, phosphoribosyl pyrophosphate synthetase 1 /DB_XREF=gi:12804406 /UG=Hs.56 phosphoribosyl pyrophosphate synthetase 1 /FEA-mRNA /PROD=phosphoribosyl pyrophosphate synthetase 1
218189_s_at	gb:NM 018946.2 /DEF=Homo sapiens N-acetylneuraminic acid phosphate synthase; sialic acid synthase (SAS), mRNA. /FEA-mRNA /GEN=SAS /PROD=N-acetylneuraminic acid phosphate synthase /DB_XREF=gi:12056472 /UG=Hs.274424 N-acetylneuraminic acid phosphate synthase; sialic acid synthase /FL=gb:NM 018946.2 gb:BC000008.1 gb:AF257466.1
200947_s_at	gb:NM 005271.1 /DEF=Homo sapiens glutamate dehydrogenase 1 (GLUD1), mRNA. /FEA-mRNA /GEN=GLUD1 /PROD=glutamate dehydrogenase 1 /DB_XREF=gi:4885280 /UG=Hs.77508 glutamate dehydrogenase 1 /FL=gb:J03248.1 gb:M37154.1 gb:M20867.1 gb:NM 005271.1
202798_at	gb:NM 006323.1 /DEF=Homo sapiens SEC24 (S. cerevisiae) related gene family, member B (SEC24B), mRNA. /FEA-mRNA /GEN=SEC24B /PROD=SEC24 (S. cerevisiae) related gene family, member B /DB_XREF=gi:5454045 /UG=Hs.7239 SEC24 (S. cerevisiae) related gene family, member B /FL=gb:NM 006323.1
205323_s_at	gb:NM 005955.1 /DEF=Homo sapiens metal-regulatory transcription factor 1 (MTF1), mRNA. /FEA-mRNA /GEN=MTF1 /PROD=metal-regulatory transcription factor 1 /DB_XREF=gi:5174588 /UG=Hs.211581 metal-regulatory transcription factor 1 /FL=gb:NM 005955.1
212622_at	Consensus includes gb:N64760 /FEA-EST /DB_XREF=gi:1212589 /DB_XREF=est:y230c06.s1 /CLONE=IMAGE:284554 /UG=Hs.174905 KIAA0033 protein
212033_at	Consensus includes gb:BF055107 /FEA-EST /DB_XREF=gi:10809003 /DB_XREF=est:7j75a05.x1 /CLONE=IMAGE:3392240 /UG=Hs.180789 S164 protein
218919_at	gb:NM 024699.1 /DEF=Homo sapiens hypothetical protein FLJ14007 (FLJ14007), mRNA. /FEA-mRNA /GEN=FLJ14007 /PROD=hypothetical protein FLJ14007 /DB_XREF=gi:13375984 /UG=Hs.99519 hypothetical protein FLJ14007 /FL=gb:NM 024699.1
209271_at	gb:AB032251.1 /DEF=Homo sapiens BPTF mRNA for bromodomain PHD finger transcription factor, complete cds. /FEA-mRNA /GEN=BPTF /PROD=bromodomain PHD finger transcription factor /DB_XREF=gi:6683491 /UG=Hs.99872 fetal Alzheimer antigen /FL=gb:AB032251.1
213322_at	Consensus includes gb:AL031778 /DEF=Human DNA sequence from clone 34B21 on chromosome 6p12.1-21.1. Contains part of a gene for a novel protein with ZU5 domain similar to part of Tight Junction Protein Z01 (TJPL1) and UNC5 Homologs, the gene for a novel benzodiazapine... /FEA-mRNA 2 /DB_XREF=gi:4153958 /UG=Hs.183056 Human DNA sequence from clone 34B21 on chromosome 6p12.1-21.1. Contains part of a novel protein with ZU5 domain similar to part of Tight Junction Protein Z01 (TJPL1) and UNC5 Homologs, the gene for a novel benzodiazapine receptor
221895_at	Consensus includes gb:AW469184 /FEA-EST /DB_XREF=gi:7039290 /DB_XREF=est:hc78g04.x1 /CLONE=IMAGE:2898870 /UG=Hs.65406 ESTs
217760_at	Consensus includes gb:AA176780 /FEA-EST /DB_XREF=gi:1757929 /DB_XREF=est:zp32a10.s1 /CLONE=IMAGE:611130 /UG=Hs.14512 DIPB protein /FL=gb:NM 017583.1
201448_at	Consensus includes gb:AL046419 /FEA-EST /DB_XREF=gi:5434493 /DB_XREF=est:DKEZp434N247_s1 /CLONE=DKEZp434N247 /UG=Hs.239489 TIAL cytotoxic granule-associated RNA-binding protein /FL=gb:NM 022037.1 gb:M77142.1
218465_at	gb:NM 018126.1 /DEF=Homo sapiens hypothetical protein FLJ10525 (FLJ10525), mRNA. /FEA-mRNA /GEN=FLJ10525 /PROD=hypothetical protein FLJ10525 /DB_XREF=gi:8922490 /UG=Hs.31082 hypothetical protein FLJ10525 /FL=gb:BC000948.1 gb:NM 018126.1
212880_at	Consensus includes gb:AB011113.1 /DEF=Homo sapiens mRNA for KIAA0541 protein, partial cds. /FEA-mRNA /GEN=KIAA0541 /PROD=KIAA0541 protein /DB_XREF=gi:3043605 /UG=Hs.10881 WD repeat domain 7
218142_s_at	gb:NM 016302.1 /DEF=Homo sapiens protein x 0001 (LOC511185), mRNA. /FEA-mRNA /GEN=LOC511185 /PROD=protein x 0001 /DB_XREF=gi:10047097 /UG=Hs.18925 protein x 0001 /FL=gb:NM 016302.1 gb:AF117230.1
202078_at	gb:NM 003653.1 /DEF=Homo sapiens COP9 (constitutive photomorphogenic, Arabidopsis, homolog) subunit 3 (COPS3), mRNA. /FEA-mRNA /GEN=COPS3 /PROD=COP9 (constitutive photomorphogenic, Arabidopsis, homolog) subunit 3 /DB_XREF=gi:4502974 /UG=Hs.6076 COP9 (constitutive photomorpho-

	genic, Arabidopsis, homolog) subunit 3 /FL=gb:BC001891.1 gb:AF031647.1 gb:AF03653.1 gb:AF098109.1
219069_at	gb:NM_017704.1 /DEF=Homo sapiens hypothetical protein FLJ20189 (FLJ20189), mRNA. /FEA=mrna /GEN=FLJ20189 /PROD=hypothetical protein FLJ20189 /DB_XREF=gi:18923180 /UG=Hs.29052 hypothetical protein FLJ20189 /FL=gb:NM_017704.1
218333_at	gb:NM_016041.1 /DEF=Homo sapiens CGI-101 protein (LOC51009), mRNA. /FEA=mrna /GEN=LOC51009 /PROD=CGI-101 protein /DB_XREF=gi:7705603 /UG=Hs.286131 CGI-101 protein /FL=gb:AF132289.1 gb:AF151859.1 gb:NM_016041.1 gb:AF242523.1
213082_s_at	Consensus includes gb:AJ005866.1 /DEF=Homo sapiens mRNA for putative Sqv-7-like protein, partial. /FEA=mrna /PROD=Sqv-7-like protein /DB_XREF=gi:4008516 /UG=Hs.90078 nucleotide-sugar transporter similar to C. elegans sqv-7
221452_s_at	gb:NM_030969.1 /DEF=Homo sapiens hypothetical protein MGC1223 (MGC1223), mRNA. /FEA=CDS /GEN=MGC1223 /PROD=hypothetical protein MGC1223 /DB_XREF=gi:13624338 /FL=gb:NM_030969.1
213733_at	Consensus includes gb:BF740152 /FEA=EST /DB_XREF=gi:12066828 /DB_XREF=est:n13g08.x1 /CLONE=IMAGE:3564495 /UG=Hs.121555 myosin IE
201225_s_at	gb:NM_005839.1 /DEF=Homo sapiens SerArg-related nuclear matrix protein (plenty of prolines 101-like) (SRM160), mRNA. /FEA=mrna /GEN=SRM160 /PROD=SerArg-related nuclear matrix protein (plenty of prolines 101-like) /DB_XREF=gi:5032118 /UG=Hs.18192 SerArg-related nuclear matrix protein (plenty of prolines 101-like) /FL=gb:AF049977.1 gb:NM_005839.1
219392_x_at	gb:NM_018304.1 /DEF=Homo sapiens hypothetical protein FLJ11029 (FLJ11029), mRNA. /FEA=mrna /GEN=FLJ11029 /PROD=hypothetical protein FLJ11029 /DB_XREF=gi:8922831 /UG=Hs.274448 hypothetical protein FLJ11029 /FL=gb:NM_018304.1
219212_at	gb:NM_016299.1 /DEF=Homo sapiens heat shock protein hsp70-related protein (LOC51182), mRNA. /FEA=mrna /GEN=LOC51182 /PROD=heat shock protein hsp70-related protein /DB_XREF=gi:10047093 /UG=Hs.44591 heat shock protein hsp70-related protein /FL=gb:NM_016299.1 gb:AF112210.1
217907_at	gb:NM_014161.1 /DEF=Homo sapiens HSPC071 protein (HSPC071), mRNA. /FEA=mrna /GEN=HSPC071 /PROD=HSPC071 protein /DB_XREF=gi:7661777 /UG=Hs.23038 HSPC071 protein /FL=gb:AF136633.1 gb:BC001623.1 gb:AF161556.1 gb:NM_014161.1
200727_s_at	Consensus includes gb:AA699583 /FEA=EST /DB_XREF=gi:2703730 /DB_XREF=est:zi42g07.s1 /CLONE=IMAGE:433500 /UG=Hs.42915 ARP2 (actin-related protein 2, yeast) homolog /FL=gb:AF006082.1 gb:NM_005722.1
209068_at	gb:DB9678.1 /DEF=Homo sapiens mRNA for A+U-rich element RNA binding factor, complete cds. /FEA=mrna /PROD=A+U-rich element RNA binding factor /DB_XREF=gi:3218539 /UG=Hs.170311 heterogeneous nuclear ribonucleoprotein D-like /FL=gb:DB9092.1 gb:DB9678.1
46256_at	Cluster Incl. AA522670:n139a05.s1 Homo sapiens cDNA, 3' end /CLONE=IMAGE-979184 /CLONE_end=3 /gb:AA522670 /gi:2263382 /ug=Hs.7247 /len=684
218068_s_at	gb:NM_024836.1 /DEF=Homo sapiens hypothetical protein FLJ22301 (FLJ22301), mRNA. /FEA=mrna /GEN=FLJ22301 /PROD=hypothetical protein FLJ22301 /DB_XREF=gi:13376246 /UG=Hs.181406 hypothetical protein FLJ22301 /FL=gb:NM_024836.1
208843_s_at	gb:BC001408.1 /DEF=Homo sapiens, clone MGC:1233, mRNA, complete cds. /FEA=mrna /PROD=Unknown (protein for MGC:1233) /DB_XREF=gi:12655112 /UG=Hs.6880 DKFZP434D156 protein /FL=gb:BC001408.1
202869_at	gb:NM_016816.1 /DEF=Homo sapiens 2,5-oligoadenylate synthetase 1 (40-46 kD) (OAS1), transcript variant E18, mRNA. /FEA=mrna /GEN=OAS1 /PROD=2,5-oligoadenylate synthetase 1, isoform E18 /DB_XREF=gi:8051620 /UG=Hs.82396 2,5-oligoadenylate synthetase 1 (40-46 kD) /FL=gb:NM_016816.1
213546_at	Consensus includes gb:AL050378.1 /DEF=Homo sapiens mRNA; cDNA DKFZp586I1420 (from clone DKFZp586I1420); partial cds. /FEA=mrna /GEN=DKFZp586I1420 /PROD=hypothetical protein /DB_XREF=gi:4914581 /UG=Hs.112423 Homo sapiens mRNA; cDNA DKFZp586I1420 (from clone DKFZp586I1420); partial cds
214789_x_at	Consensus includes gb:AA524274 /FEA=EST /DB_XREF=gi:2265202 /DB_XREF=est:ng34d08.s1 /CLONE=IMAGE:936687 /UG=Hs.155160 Splicing factor, arginineserine-rich, 46kD
213649_at	Consensus includes gb:AA524053 /FEA=EST /DB_XREF=gi:2264981 /DB_XREF=est:ng33b07.s1 /CLONE=IMAGE:936565 /UG=Hs.184167 splicing factor, arginineserine-rich 7 (35kD)
212251_at	Consensus includes gb:AL972475 /FEA=EST /DB_XREF=gi:5769391 /DB_XREF=est:wr40b09.x1 /CLONE=IMAGE:2490137 /UG=Hs.243901 Homo sapiens cDNA FLJ20738 fis, clone HEP08257
209166_s_at	gb:168567.1 /DEF=Human lysosomal acid alpha-mannosidase mRNA, complete cds. /FEA=mrna /PROD=lysosomal acid alpha-mannosidase /DB_XREF=gi:1658373 /UG=Hs.279854 mannosidase, alpha, class 2B, member 1 /FL=gb:NM_000528.1 gb:BC000736.1 gb:U05572.1 gb:U068567.1
200683_s_at	Consensus includes gb:BE964689 /FEA=EST /DB_XREF=gi:11768267 /DB_XREF=est:601658226r1 /CLONE=IMAGE:3885630 /UG=Hs.108104 ubiqlitin-conjugating enzyme E2L 3 /FL=gb:NM_003347.1
219913_s_at	gb:NM_016652.2 /DEF=Homo sapiens CGI-201 protein (LOC51340), mRNA. /FEA=mrna /GEN=LOC51340 /PROD=CGI-201 protein /DB_XREF=gi:11072090 /UG=Hs.268281 crooked neck protein (cnr) /FL=gb:AF255443.2 gb:NM_016652.2 gb:AF318302.1
218104_at	gb:NM_017746.1 /DEF=Homo sapiens hypothetical protein FLJ20287 (FLJ20287), mRNA. /FEA=mrna /GEN=FLJ20287 /PROD=hypothetical protein FLJ20287 /DB_XREF=gi:8923268 /UG=Hs.26369 hypothetical protein FLJ20287 /FL=gb:NM_017746.1

212345_s_at	Consensus includes gb:BE675139 /FEA=EST /DB_XREF=gi:10035680 /DB_XREF=est:7f03b12.x1 /CLONE=IMAGE:3293567 /UG=Hs.13659 hypothetical protein DKFZp586f2423
213982_s_at	Consensus includes gb:BG107203 /FEA=EST /DB_XREF=gi:12601049 /DB_XREF=est:602290933F1 /CLONE=IMAGE:4385577 /UG=Hs.13659 hypothetical protein DKFZp586f2423
202519_at	gb:NM_014938.1 /DEF=Homo sapiens KIAA0867 protein (MONDOA), mRNA. /FEA=mrna /GEN=MONDOA /PROD=MONDOA protein /DB_XREF=gi:7662347 /UG=Hs.52081 KIAA0867 protein /FL=gb:AB020674.1 gb:NM_014938.1
202892_at	gb:NM_004661.1 /DEF=Homo sapiens CDC23 (cell division cycle 23, yeast, homolog) (CDC23), mRNA. /FEA=mrna /GEN=CDC23 /PROD=cell division cycle 23, yeast homolog; CDC23 /DB_XREF=gi:4757947 /UG=Hs.135346 CDC23 (cell division cycle 23, yeast, homolog) /FL=gb:AF053977.1 gb:AB011472.1 gb:NM_004661.1 gb:AF191341.1
213876_x_at	Consensus includes gb:AW089594 /FEA=EST /DB_XREF=gi:6046928 /DB_XREF=est:xd20f04.x1 /CLONE=IMAGE:2594335 /UG=Hs.171909 U2 small nuclear ribonucleoprotein auxiliary factor, small subunit 2
202054_s_at	gb:NM_000382.1 /DEF=Homo sapiens aldehyde dehydrogenase 3 family, member A2 (ALDH3A2), mRNA. /FEA=mrna /GEN=ALDH3A2 /PROD=aldehyde dehydrogenase 3A2 /DB_XREF=gi:4557302 /UG=Hs.159608 aldehyde dehydrogenase 3 family, member A2 /FL=gb:U47162.1 gb:U46689.1 gb:NM_000382.1 gb:AF167438.1 /DEF=Homo sapiens androgen-regulated short-chain dehydrogenase/reductase 1 (ARSDR1), mRNA, complete cds. /FEA=mrna /GEN=ARSDR1 /PROD=androgen-regulated short-chain dehydrogenase/reductase 1 /DB_XREF=gi:9622123 /UG=Hs.179817 CGI-82 protein /FL=gb:BC000112.1 gb:AF151840.1 gb:NM_016026.1 gb:AF167438.1
208758_at	gb:D89976.1 /DEF=Homo sapiens mRNA for 5-aminimidazole-4-carboxamide ribonucleotide transformylase, complete cds. /FEA=mrna /PROD=5-aminimidazole-4-carboxamide ribonucleotide transformylase /DB_XREF=gi:2317691 /UG=Hs.90280 5-aminimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase /FL=gb:U37436.1 gb:D82348.1 gb:D89976.1 gb:NM_004044.1
212749_s_at	Consensus includes gb:AI096477 /FEA=EST /DB_XREF=gi:3445971 /DB_XREF=est:qa03c06.x1 /CLONE=IMAGE:1685674 /UG=Hs.48297 DKFZP586C1620 protein
200890_s_at	Consensus includes gb:AW006345 /FEA=EST /DB_XREF=gi:5855123 /DB_XREF=est:wt04d05.x1 /CLONE=IMAGE:2506473 /UG=Hs.250773 signal sequence receptor, alpha (translocon-associated protein alpha) /FL=gb:AF156965.1 gb:NM_003144.2
211675_s_at	gb:AF054589.1 /DEF=Homo sapiens HIC protein isoform p40 and HIC protein isoform p32 mRNAs, complete cds. /FEA=mrna /PROD=HIC protein isoform p32; HIC protein isoform p40 /DB_XREF=gi:3426297 /FL=gb:AF054589.1
206792_x_at	gb:NM_000923.1 /DEF=Homo sapiens phosphodiesterase 4C, cAMP-specific (dunce (Drosophila)-homolog phosphodiesterase E1) (PDE4C), mRNA. /FEA=mrna /GEN=PDE4C /PROD=phosphodiesterase 4C, cAMP-specific (dunce (Drosophila)-homolog phosphodiesterase E1) /DB_XREF=gi:4505664 /UG=Hs.189 phosphodiesterase 4C, cAMP-specific (dunce (Drosophila)-homolog phosphodiesterase E1) /FL=gb:NM_000923.1
218718_at	gb:NM_016205.1 /DEF=Homo sapiens platelet derived growth factor C (PDGFC), mRNA. /FEA=mrna /GEN=PDGFC /PROD=secretory growth factor-like protein fallotelin /DB_XREF=gi:9994186 /UG=Hs.43080 platelet derived growth factor C /FL=gb:AF091434.1 gb:AF244813.1 gb:AB033831.1 gb:NM_016205.1
201742_x_at	gb:NM_006924.1 /DEF=Homo sapiens splicing factor, arginineserine-rich 1 (splicing factor 2, alternate splicing factor) (SFRS1), mRNA. /FEA=mrna /GEN=SFRS1 /PROD=splicing factor, arginineserine-rich 1 (splicing factor 2, alternate splicing factor) /DB_XREF=gi:5902075 /UG=Hs.73737 splicing factor, arginineserine-rich 1 (splicing factor 2, alternate splicing factor) /FL=gb:M69040.1 gb:NM_006924.1
218622_at	gb:NM_024057.1 /DEF=Homo sapiens hypothetical protein MGC5585 (MGC5585), mRNA. /FEA=mrna /GEN=MGC5585 /PROD=hypothetical protein MGC5585 /DB_XREF=gi:13129027 /UG=Hs.5152 hypothetical protein MGC5585 /FL=gb:BC000861.1 gb:NM_024057.1
212176_at	Consensus includes gb:AA902326 /FEA=EST /DB_XREF=gi:3037233 /DB_XREF=est:ok92b01.s1 /CLONE=IMAGE:1521385 /UG=Hs.18368 DKFZP564B0769 protein
218970_s_at	gb:NM_015960.1 /DEF=Homo sapiens CGI-32 protein (LOC51076), mRNA. /FEA=mrna /GEN=LOC51076 /PROD=CGI-32 protein /DB_XREF=gi:7705727 /UG=Hs.16606 CGI-32 protein /FL=gb:AF132966.1 gb:NM_015960.1
201696_at	gb:NM_005626.1 /DEF=Homo sapiens splicing factor, arginineserine-rich 4 (SFRS4), mRNA. /FEA=mrna /GEN=SFRS4 /PROD=splicing factor, arginineserine-rich 4 /DB_XREF=gi:5032088 /UG=Hs.76122 splicing factor, arginineserine-rich 4 /FL=gb:BC002781.1 gb:U4076.1 gb:NM_005626.1
222103_at	Consensus includes gb:AI434345 /FEA=EST /DB_XREF=gi:4295529 /DB_XREF=est:ti48b06.x1 /CLONE=IMAGE:2133663 /UG=Hs.36908 activating transcription factor 1 /FL=gb:NM_005171.1
204036_at	Consensus includes gb:AW269335 /FEA=EST /DB_XREF=gi:6656365 /DB_XREF=est:xs47d05.x1 /CLONE=IMAGE:2772777 /UG=Hs.75794 endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 2 /FL=gb:U78192.1 gb:U80811.1 gb:NM_001401.1
218283_at	gb:NM_016305.1 /DEF=Homo sapiens k1aa-iso protein (LOC51188), mRNA. /FEA=mrna /GEN=LOC51188 /PROD=k1aa-iso protein /DB_XREF=gi:10047103 /UG=Hs.9774 k1aa-iso protein /FL=gb:NM_016305.1 gb:AF201950.1
209654_at	gb:BC004902.1 /DEF=Homo sapiens, clone MGC:4271, mRNA, complete cds. /FEA=mrna /PROD=Unknown (protein for MGC:4271) /DB_XREF=gi:13436178 /UG=Hs.5070 KIAA0947 protein /FL=gb:BC004902.1

209083_at	gb:U34690.1 /DEF=Human coronin-like protein (HCOR01) mRNA, complete cds. /FEA=mrna /GEN=HCOR01 /PROD=coronin-like protein /DB_XREF=gi:1002922 /UG=Hs.109606 coronin, actin-binding protein, 1A /FL=gb:U34690.1 gb:NM 007074.1 gb:D44497.1
221873_at	Consensus includes gb:AW162015 /FEA=EST /DB_XREF=gi:6301048 /DB_XREF=est:au72409.x1 /CLONE=IMAGE:2781809 /UG=Hs.154095 zinc finger protein 143 (clone PH2-1)
213573_at	Consensus includes gb:AA861608 /FEA=EST /DB_XREF=gi:2953748 /DB_XREF=est:ak34601.s1 /CLONE=IMAGE:1407864 /UG=Hs.180446 karyopherin (importin) beta 1
209580_s_at	gb:AF114784.1 /DEF=Homo sapiens methyl-CpG binding endonuclease (MED1) mRNA, complete cds. /FEA=mrna /GEN=MED1 /PROD=methyl-CpG binding endonuclease /DB_XREF=gi:4539758 /UG=Hs.35947 methyl-CpG binding domain protein 4 /FL=gb:AF114784.1 gb:NM 003925.1 gb:AF114784.1
219097_x_at	gb:NM 024104.1 /DEF=Homo sapiens hypothetical protein MGC2747 (MGC2747), mRNA. /FEA=mrna /GEN=MGC2747 /PROD=hypothetical protein MGC2747 /DB_XREF=gi:13129111 /UG=Hs.227203 hypothetical protein MGC2747 /FL=gb:BC001948.1 gb:NM 024104.1
206513_at	gb:NM 004833.1 /DEF=Homo sapiens absent in melanoma 2 (AIM2), mRNA. /FEA=mrna /GEN=AIM2 /PROD=absent in melanoma 2 /DB_XREF=gi:4757733 /UG=Hs.105115 absent in melanoma 2 /FL=gb:AF024714.1 gb:NM 004833.1
209268_at	gb:AF165513.1 /DEF=Homo sapiens vacuolar protein sorting 45 isoform (VPS45) mRNA, complete cds. /FEA=mrna /GEN=VPS45 /PROD=vacuolar protein sorting 45 isoform /DB_XREF=gi:9294732 /UG=Hs.6650 vacuolar protein sorting 45B (yeast homolog) /FL=gb:NM 007259.1 gb:AF165513.1
219329_s_at	gb:NM 016085.1 /DEF=Homo sapiens apoptosis related protein APR-3 (APR-3), mRNA. /FEA=mrna /GEN=APR-3 /PROD=apoptosis related protein APR-3 /DB_XREF=gi:7706360 /UG=Hs.9527 apoptosis related protein APR-3 /FL=gb:AF144055.2 gb:NM 016085.1
202051_s_at	DB_XREF=gi:7706360 /UG=Hs.9527 apoptosis related protein APR-3 (APR-3), mRNA. /FEA=mrna /GEN=ZNF262 /PROD=zinc finger protein 262
200749_at	gb:NM 005095.1 /DEF=Homo sapiens zinc finger protein 262 (ZNF262), mRNA. /FEA=mrna /GEN=ZNF262 /PROD=zinc finger protein 262
213373_s_at	UG=Hs.150390 zinc finger protein 262 /FL=gb:AB007885.1 gb:NM 005095.1
212673_at	Consensus includes gb:BF112006 /FEA=EST /DB_XREF=gi:10941619 /DB_XREF=est:7137e05.x1 /CLONE=IMAGE:3523665 /UG=Hs.10842 RAN, member RAS oncogene family /
200749_at	Consensus includes gb:BC004272.1 gb:M31469.1 gb:AF052578.1 gb:AF054183.1 gb:NM 006325.2
213373_s_at	FL=gb:BC000852.1 gb:NM 006325.2
213373_s_at	Consensus includes gb:BF439983 /FEA=EST /DB_XREF=gi:11452500 /DB_XREF=est:nac51f11.x1 /CLONE=IMAGE:3406220 /UG=Hs.19949 caspase 8, apopto-sis-related
212673_at	cysteine protease /FL=gb:U58143.1
201771_at	Consensus includes gb:D42084.1 /DEF=Human mRNA for KIAA0094 gene, partial cds. /FEA=mrna /GEN=KIAA0094 /DB_XREF=gi:577314 /UG=Hs.82007 KIAA0094 protein
209607_x_at	gb:NM 005698.1 /DEF=Homo sapiens secretory carrier membrane protein 3 (SCAMP3), mRNA. /FEA=mrna /GEN=SCAMP3 /PROD=secretory carrier membrane protein 3 /DB_XREF=gi:5032076 /UG=Hs.20060 secretory carrier membrane protein 3 /FL=gb:BC000161.2 gb:BC0005135.1 gb:AF005039.1
217317_s_at	gb:NM 005698.1 /DEF=Human thermolabile (monoamine, M form) phenol sulfotransferase (STM) mRNA, complete cds. /FEA=mrna /GEN=STM /PROD=thermolabile (monoamine, M form) phenol sulfotransferase /DB_XREF=gi:468256 /UG=Hs.274614 sulfotransferase family, cytosolic, 1A, phenol-preferring, member 3 /FL=gb:NM 003166.1 gb:L19956.1 gb:U34199.1 gb:U08032.1
202272_s_at	Consensus includes gb:AB002391.2 /DEF=Homo sapiens mRNA for KIAA0393 protein, partial cds. /FEA=mrna /GEN=KIAA0393 /PROD=KIAA0393 protein /DB_XREF=gi:6683696 /UG=Hs.266933 hec domain and RJD 2
210629_x_at	gb:NM 015176.1 /DEF=Homo sapiens KIAA0483 protein (KIAA0483), mRNA. /FEA=mrna /GEN=KIAA0483 /PROD=KIAA0483 protein /DB_XREF=gi:7662157 /UG=Hs.64691 KIAA0483 protein /FL=gb:NM 015176.1
205329_s_at	gb:AF000425.1 /DEF=Homo sapiens LST1 mRNA, clustIA splice variant, complete cds. /FEA=mrna /GEN=LST1 /DB_XREF=gi:2145065 /UG=Hs.88411 lymphocyte antigen 117 /FL=gb:AF000425.1
218194_at	gb:NM 003794.1 /DEF=Homo sapiens sorting nexin 4 (SNX4), mRNA. /FEA=mrna /GEN=SNX4 /PROD=sorting nexin 4 /DB_XREF=gi:4507144 /UG=Hs.267812 sorting nexin 4 /FL=gb:AF130078.1 gb:AF065485.1 gb:NM 003794.1
220560_at	gb:NM 015523.1 /DEF=Homo sapiens small fragment nucleases (DKFP566E144), mRNA. /FEA=mrna /GEN=DKFP566E144 /PROD=small fragment nucleases /DB_XREF=gi:7661645 /UG=Hs.7527 small fragment nucleases /FL=gb:AF151872.1 gb:AL110239.1 gb:NM 015523.1
208270_s_at	gb:NM 014144.1 /DEF=Homo sapiens SMS3 protein (SMS3), mRNA. /FEA=mrna /GEN=SMS3 /PROD=SMS3 protein /DB_XREF=gi:7662662 /UG=Hs.272100 SMS3 protein /FL=gb:AB029488.1 gb:NM 014144.1
220175_s_at	gb:NM 020216.2 /DEF=Homo sapiens arginyl aminopeptidase (aminopeptidase B) (RNPEP), mRNA. /FEA=mrna /GEN=RNPEP /PROD=arginyl aminopeptidase (aminopeptidase B) /DB_XREF=gi:13443030 /UG=Hs.283667 arginyl aminopeptidase (aminopeptidase B) /FL=gb:NM 020216.2
212429_s_at	gb:NM 020667.1 /DEF=Homo sapiens hypothetical protein from clone 1659351 (LOC57397), mRNA. /FEA=mrna /GEN=LOC57397 /PROD=hypothetical protein from clone 1659351 /DB_XREF=gi:10190707 /UG=Hs.288838 hypothetical protein from clone 1659351 /FL=gb:NM 020667.1
	Consensus includes gb:AW194657 /FEA=EST /DB_XREF=gi:6473537 /DB_XREF=est:xb28b12.x1 /CLONE=IMAGE:2577599 /UG=Hs.75782 general transcription factor IIIC, polypeptide 2 (beta subunit, 110kd)

209058_at	gb:AB002282.1 / DEF=Homo sapiens mRNA for hMBF1alpha, complete cds. / FEA=mrna / PROD=hMBF1alpha / DB_XREF=gi:6526354 / UG=Hs.174050 endothelial differentiation-related factor 1 / FL=gb:NM_003792.1 gb:AB002282.1
212535_at	Consensus includes gb:AA142929 / FEA=EST / DB_XREF=gi:1712307 / DB_XREF=est:z140q07.s1 / CLONE=IMAGE:504444 / UG=Hs.288993 ESTs
201524_x_at	gb:NM_003348.1 / DEF=Homo sapiens ubiquitin-conjugating enzyme E2N (homologous to yeast UBC13) (UBE2N), mRNA. / FEA=mrna / GEN=UBC2N / PROD=ubiquitin-conjugating enzyme E2N (homologous to yeast UBC13) / FL=gb:BC000396.1 gb:BC0003365.1 gb:NM_003348.1
201716_at	gb:NM_003099.1 / DEF=Homo sapiens sorting nexin 1 (SNX1), mRNA. / FEA=mrna / GEN=SNX1 / PROD=sorting nexin 1 / DB_XREF=gi:4507138 / UG=Hs.75283
213097_s_at	sorting nexin 1 / FL=gb:BC000357.1 gb:U53225.1 gb:AF065483.1 gb:NM_003099.1 Consensus includes gb:AI338837 / FEA=EST / DB_XREF=gi:4075764 / DB_XREF=est:qq28f09.x1 / CLONE=IMAGE:1933865 / UG=Hs.82254 zototin related factor 1
213532_at	Consensus includes gb:AI797833 / FEA=EST / DB_XREF=gi:5363390 / DB_XREF=est:wh79e10.x1 / CLONE=IMAGE:2386986 / UG=Hs.52438 ESTs, Weakly similar to ORF YOR126c S.cerevisiae
210766_s_at	gb:AF053640.1 / DEF=Homo sapiens trachea cellular apoptosis susceptibility protein (CSE1), mRNA, complete cds. / FEA=mrna / GEN=CSE1 / PROD=cellular apoptosis susceptibility protein / DB_XREF=gi:3560554 / UG=Hs.90073 chromosome segregation 1 (yeast homolog)-like / FL=gb:AF053640.1
209523_at	Consensus includes gb:AK001618.1 / DEF=Homo sapiens cDNA FLJ10756 fis, clone NT2RP3004572, highly similar to Homo sapiens cofactor of initiator function mRNA. / FEA=mrna / DB_XREF=gi:7022983 / UG=Hs.122752 TATA box binding protein (TBP)-associated factor, RNA polymerase II, B, 150KD / FL=gb:AF026445.1 gb:AF040701.1 gb:AF057694.1 gb:NM_003184.1
209276_s_at	gb:AF162769.1 / DEF=Homo sapiens thioltransferase mRNA, complete cds. / FEA=mrna / PROD=thioltransferase / DB_XREF=gi:5442445 / UG=Hs.28988
200848_at	glutaredoxin (thioltransferase) / FL=gb:BC005304.1 gb:AF162769.1 gb:D21238.1 Consensus includes gb:AA479488 / FEA=EST / DB_XREF=gi:2208044 / DB_XREF=est:zv21c09.s1 / CLONE=IMAGE:754288 / UG=Hs.4113 S-adenosylhomocysteine hydrolase-like 1 / FL=gb:U82761.1 gb:NM_006621.1
212406_s_at	Consensus includes gb:AB028973.1 / DEF=Homo sapiens mRNA for KIAA1050 protein, partial cds. / FEA=mrna / GEN=KIAA1050 / PROD=KIAA1050 protein / DB_XREF=gi:5689436 / UG=Hs.184628 hypothetical protein FLJ10883
212072_s_at	Consensus includes gb:AL049761 / DEF=Human DNA sequence from clone RP5-863C7 on chromosome 20p12.3-13. Contains the CSNK2A1 gene for casein kinase 2 alpha 1 polypeptide (EC 2.7.1.37), ESTs, STSs and GSSs / FEA=mrna_2 / DB_XREF=gi:5738437 / UG=Hs.155140 casein kinase 2, alpha 1 polypeptide
203159_at	gb:NM_014905.1 / DEF=Homo sapiens glutaminase (GLS), mRNA. / FEA=mrna / GEN=GLS / PROD=glutaminase C / DB_XREF=gi:7662327 / UG=Hs.239189 glutaminase / FL=gb:AF327434.1 gb:AB020645.1 gb:AF097493.1 gb:AF223943.1 gb:NM_014905.1
203521_s_at	gb:NM_014345.1 / DEF=Homo sapiens endocrine regulator (HRIHFB2436), mRNA. / FEA=mrna / GEN=HRIHFB2436 / PROD=endocrine regulator / DB_XREF=gi:7657183 / UG=Hs.48433 endocrine regulator / FL=gb:AF121141.1 gb:NM_014345.1
204439_at	gb:NM_006820.1 / DEF=Homo sapiens hypothetical protein, expressed in osteoblast (GS3686), mRNA. / FEA=mrna / GEN=GS3686 / PROD=hypothetical protein, expressed in osteoblast / DB_XREF=gi:5803026 / UG=Hs.75470 hypothetical protein, expressed in osteoblast / FL=gb:AB000115.1 gb:NM_006820.1
218646_at	gb:NM_017867.1 / DEF=Homo sapiens hypothetical protein FLJ20534 (FLJ20534), mRNA. / FEA=mrna / GEN=FLJ20534 / PROD=hypothetical protein / FL=gb:AF20534 / DB_XREF=gi:8923502 / UG=Hs.44344 hypothetical protein FLJ20534 / FL=gb:AL136673.1 gb:NM_017867.1
213168_at	Consensus includes gb:AUI45005 / FEA=EST / DB_XREF=gi:11006526 / DB_XREF=est:AUI45005 / CLONE=HEMRA1003603 / UG=Hs.44450 Sp3 transcription factor
210371_s_at	gb:BC003092.1 / DEF=Homo sapiens, similar to retinoblastoma binding protein 4, clone MGC:1393, mRNA, complete cds. / FEA=mrna / PROD=Similar to retinoblastoma binding protein 4 / DB_XREF=gi:13111850 / UG=Hs.16003 retinoblastoma-binding protein 4 / FL=gb:BC003092.1 gb:NM_005610.1
200052_s_at	gb:NM_004515.1 / DEF=Homo sapiens interleukin enhancer binding factor 2, 45KD (ILF2), mRNA. / FEA=mrna / GEN=ILF2 / PROD=interleukin enhancer binding factor 2, 45kd / DB_XREF=gi:4758601 / UG=Hs.75117 interleukin enhancer binding factor 2, 45KD / FL=gb:BC000382.1 gb:NM_004515.1 gb:U10323.1
201019_s_at	gb:NM_001412.1 / DEF=Homo sapiens eukaryotic translation initiation factor 1A (EIF1A), mRNA. / FEA=mrna / GEN=EIF1A / PROD=eukaryotic translation initiation factor 1A / DB_XREF=gi:4503498 / UG=Hs.4310 eukaryotic translation initiation factor 1A / FL=gb:BC000793.1 gb:U18960.1 gb:NM_001412.1
219892_at	gb:NM_023003.1 / DEF=Homo sapiens transmembrane 6 superfamily member 1 (TM6SF1), mRNA. / FEA=mrna / GEN=TM6SF1 / PROD=transmembrane 6 superfamily member 1 / DB_XREF=gi:13194198 / UG=Hs.133865 transmembrane 6 superfamily member 1 / FL=gb:AF255922.1 gb:NM_023003.1
218095_s_at	gb:NM_018475.1 / DEF=Homo sapiens uncharacterized hypothalamus protein HTPMP (LOC55858), mRNA. / FEA=mrna / GEN=LOC55858 / PROD=uncharacterized hypothalamus protein HTPMP / DB_XREF=gi:8923860 / UG=Hs.236510 uncharacterized hypothalamus protein HTPMP / FL=gb:BC003545.1 gb:AF220188.1 gb:NM_018475.1 gb:AF183409.1

218042_at	gb:NM_016129.1 /DEF=Homo sapiens COP9 complex subunit 4 (LOC51136), mRNA. /FEA=mrna /GEN=LOC51136 /PROD=COP9 complex subunit 4 /DB_XREF=gi:7705844 /UG=Hs.6671 COP9 complex subunit 4 /FL=gb:BC004302.1 gb:AF100757.1 gb:NM_016129.1
202172_at	Consensus includes gb:BG035116 /FEA=EST /DB_XREF=gi:12428927 /DB_XREF=est:602324811F1 /CLONE=IMAGE:4412907 /UG=Hs.6557 zinc finger protein 161 /FL=gb:D28118.1 gb:NM_007146.1
218108_at	gb:NM_018108.1 /DEF=Homo sapiens hypothetical protein FLJ10483 (FLJ10483), mRNA. /FEA=mrna /GEN=FLJ10483 /PROD=hypothetical protein FLJ10483 /DB_XREF=gi:8922451 /UG=Hs.6877 hypothetical protein FLJ10483 /FL=gb:NM_018108.1
212539_at	Consensus includes gb:A1422099 /FEA=EST /DB_XREF=gi:4268030 /DB_XREF=est:tf57h09.x1 /CLONE=IMAGE:2103425 /UG=Hs.14570 hypothetical protein FLJ22550
212635_at	Consensus includes gb:AW161626 /FEA=EST /DB_XREF=gi:6300659 /DB_XREF=est:au66b11.x1 /CLONE=IMAGE:2781405 /UG=Hs.21739 Homo sapiens mRNA; cDNA DKFZp586I1518 (from clone DKFZp586I1518)
203356_at	Consensus includes gb:BE349584 /FEA=EST /DB_XREF=gi:9261437 /DB_XREF=est:ht55h12.x1 /CLONE=IMAGE:3150695 /UG=Hs.7145 calpain 7 /FL=gb:AB028639.1 gb:NM_014296.1
208174_x_at	gb:NM_005089.1 /DEF=Homo sapiens U2 small nuclear ribonucleoprotein auxiliary factor, small subunit 2 (U2AF1RS2), mRNA. /FEA=mrna /GEN=U2AF1RS2 /PROD=U2 small nuclear ribonucleoprotein auxiliary factor, small subunit 2 /DB_XREF=gi:4827045 /UG=Hs.171909 U2 small nuclear ribonucleoprotein auxiliary factor, small subunit 2 /FL=gb:D49677.1 gb:NM_005089.1
53912_at	Cluster Incl. AI668643:zb13f10.x5 Homo sapiens cDNA, 3' end /CLONE=IMAGE:301963 /clone_end=3 /gb=AI668643 /gi=4827951 /ug=Hs.15827 /len=601
221736_at	Consensus includes gb:AAL16777 /FEA=EST /DB_XREF=gi:1728392 /DB_XREF=est:z118c08.s1 /CLONE=IMAGE:502286 /UG=Hs.25431 KIAA1219 protein
209475_at	gb:AF106069.1 /DEF=Homo sapiens deubiquitinating enzyme (UNPH4) mRNA, complete cds. /FEA=mrna /GEN=UNPH4 /PROD=deubiquitinating enzyme /DB_XREF=gi:5814096 /UG=Hs.23168 ubiquitin specific protease 15 /FL=gb:AF013990.1 gb:AF106069.1
204366_s_at	gb:NM_001521.1 /DEF=Homo sapiens general transcription factor IIIC, polypeptide 2 (beta subunit, 110kD) (GTF3C2), mRNA. /FEA=mrna /GEN=GTF3C2 /PROD=general transcription factor IIIC, polypeptide 2 (beta subunit, 110kD) /DB_XREF=gi:4504204 /UG=Hs.75782 general transcription factor IIIC, polypeptide 2 (beta subunit, 110kD) /FL=gb:D13636.1 gb:NM_001521.1
212594_at	Consensus includes gb:BG260519 /FEA=EST /DB_XREF=gi:12770335 /DB_XREF=est:602372005F1 /CLONE=IMAGE:4480024 /UG=Hs.129952 KIAA0560 gene product
212140_at	Consensus includes gb:AB014548.1 /DEF=Homo sapiens mRNA for KIAA0648 protein, partial cds. /FEA=mrna /GEN=KIAA0648 /PROD=KIAA0648 protein /DB_XREF=gi:3327109 /UG=Hs.31921 KIAA0648 protein
219083_at	gb:NM_018130.1 /DEF=Homo sapiens hypothetical protein FLJ10539 (FLJ10539), mRNA. /FEA=mrna /GEN=FLJ10539 /PROD=hypothetical protein FLJ10539 /DB_XREF=gi:8922499 /UG=Hs.93391 hypothetical protein FLJ10539 /FL=gb:NM_018130.1
215772_x_at	Consensus includes gb:AL050226.1 /DEF=Homo sapiens mRNA: cDNA DKFZp586M2023 (from clone DKFZp586M2023); partial cds. /FEA=mrna /GEN=DKFZp586M2023 /PROD=hypothetical protein /DB_XREF=gi:4884469 /UG=Hs.247309 succinate-CoA ligase, GDP-forming, beta subunit
216194_s_at	Consensus includes gb:AD001527 /DEF=Homo sapiens DNA from chromosome 19-cosmid f24590 containing CAPNS and POL2RI, genomic sequence /FEA=CDS 3 /DB_XREF=gi:1905899 /UG=Hs.31053 cytoskeleton-associated protein 1
204373_s_at	gb:NM_014810.1 /DEF=Homo sapiens KIAA0480 gene product (KIAA0480), mRNA. /FEA=mrna /GEN=KIAA0480 /PROD=KIAA0480 gene product /DB_XREF=gi:7662155 /UG=Hs.92200 KIAA0480 gene product /FL=gb:AB007949.1 gb:NM_014810.1
208927_at	Consensus includes gb:BF673888 /FEA=EST /DB_XREF=gi:11947783 /DB_XREF=est:602137554F1 /CLONE=IMAGE:4274077 /UG=Hs.129951 speckle-type POZ protein /FL=gb:BC001269.1
220146_at	gb:NM_016562.1 /DEF=Homo sapiens toll-like receptor 7 (LOC51284), mRNA. /FEA=mrna /GEN=LOC51284 /PROD=toll-like receptor 7 /DB_XREF=gi:7706092 /UG=Hs.179152 toll-like receptor 7 /FL=gb:AF240467.1 gb:NM_016562.1 gb:AF245702.1
219694_at	gb:NM_019018.1 /DEF=Homo sapiens hypothetical protein (FLJ11127), mRNA. /FEA=mrna /GEN=FLJ11127 /PROD=hypothetical protein /DB_XREF=gi:9506640 /UG=Hs.91165 hypothetical protein /FL=gb:NM_019018.1
213229_at	Consensus includes gb:BF590131 /FEA=EST /DB_XREF=gi:11682455 /DB_XREF=est:nab19e04.x1 /CLONE=IMAGE:3266383 /UG=Hs.87889 helicase-moi
214356_s_at	Consensus includes gb:AI272899 /FEA=EST /DB_XREF=gi:3895167 /DB_XREF=est:ql47c07.x1 /CLONE=IMAGE:1875468 /UG=Hs.3852 KIAA0368 protein
213153_at	Consensus includes gb:AB028999.1 /DEF=Homo sapiens mRNA for KIAA1076 protein, partial cds. /FEA=mrna /GEN=KIAA1076 /PROD=KIAA1076 protein /DB_XREF=gi:5689488 /UG=Hs.154525 KIAA1076 protein
218294_s_at	gb:AF267865.1 /DEF=Homo sapiens DC41 mRNA, complete cds. /FEA=mrna /PROD=DC41 /DB_XREF=gi:12006056 /UG=Hs.271623 nucleoporin 50kD /FL=gb:AF267865.1 gb:AF107840.1 gb:NM_007172.1 gb:AF116624.1
221522_at	gb:AL136784.1 /DEF=Homo sapiens mRNA: cDNA DKFZp434L0718 (from clone DKFZp434L0718); complete cds. /FEA=mrna /GEN=DKFZp434L0718 /PROD=hypothetical

205930_at	protein /DB_XREF=gi:12053080 /UG=Hs.59236 Homo sapiens mRNA; cDNA DKFZp344J0718 (from clone DKFZp344J0718); complete cds /FL=gb:AL136784.1 /GEN=U05513.1 /DEF=Homo sapiens general transcription factor IIE, polypeptide 1 (alpha subunit, 56kd) (GTF2E1), mRNA. /FEA=mrna /PROD=general transcription factor IIE, polypeptide 1 (alpha subunit, 56kd) (GTF2E1), mRNA. /FEA=mrna
210312_s_at	gb:BC002640.1 /DEF=Homo sapiens, Similar to uterine protein, clone MGC:4279, mRNA, complete cds. /FEA=mrna /PROD=Similar to uterine protein /DB_XREF=gi:12803610 /UG=Hs.4187 hypothetical protein 24636 /FL=gb:BC002640.1
213838_at	Consensus includes gb:AA191426 /FEA=EST /DB_XREF=gi:1780105 /DB_XREF=est:zp83909.s1 /CLONE=IMAGE:626848 /UG=Hs.279886 RAN binding protein 9
202520_s_at	gb:NM_000249.1 /DEF=Homo sapiens mutL (E. coli) homolog 1 (colon cancer, nonpolyposis type 2) (MLH1), mRNA. /FEA=mrna /GEN=MLH1 /PROD=mutL homolog 1 /DB_XREF=gi:4557756 /UG=Hs.57301 mutL (E. coli) homolog 1 (colon cancer, nonpolyposis type 2) /FL=gb:NM_000249.1 gb:U07343.1
221834_at	Consensus includes gb:AV700132 /FEA=EST /DB_XREF=gi:10302103 /DB_XREF=est:AV700132 /CLONE=GKCGSE03 /UG=Hs.295923 seven in absentia (Drosophila) homolog 1
210942_s_at	gb:AB022918.1 /DEF=Homo sapiens mRNA for alpha2,3-sialyltransferase ST3Gal VI, complete cds. /FEA=mrna /GEN=ST3Gal VI /PROD=alpha2,3-sialyltransferase ST3Gal VI /DB_XREF=gi:4827246 /UG=Hs.34578 alpha2,3-sialyltransferase /FL=gb:AB022918.1
202396_at	gb:NM_006706.1 /DEF=Homo sapiens transcription factor CA150 (CA150), mRNA. /FEA=mrna /GEN=CA150 /PROD=transcription factor CA150 /DB_XREF=gi:5729753 /UG=Hs.13063 transcription factor CA150 /FL=gb:AF017789.1 gb:NM_006706.1
219598_s_at	gb:NM_016104.1 /DEF=Homo sapiens PTD013 protein (PTD013), mRNA. /FEA=mrna /GEN=PTD013 /PROD=PTD013 protein /DB_XREF=gi:7706668 /UG=Hs.279857 PTD013 protein /FL=gb:AF092134.1 gb:NM_016104.1
202502_at	gb:NM_000016.1 /DEF=Homo sapiens acyl-Coenzyme A dehydrogenase, C-4 to C-12 straight chain (ACADM), nuclear gene encoding mitochondrial protein, mRNA. /FEA=mrna /GEN=ACADM /PROD=acyl-Coenzyme A dehydrogenase, C-4 to C-12 straight chain proenzyme /DB_XREF=gi:4557230 /UG=Hs.79158 acyl-Coenzyme A dehydrogenase, C-4 to C-12 straight chain /FL=gb:BC005377.1 gb:NM16827.1 gb:NM_000016.1 gb:AF251043.1
211968_s_at	Consensus includes gb:AI962933 /FEA=EST /DB_XREF=gi:5755646 /DB_XREF=est:wc25a07.x1 /CLONE=IMAGE:2508468 /UG=Hs.289088 heat shock 90kd protein 1, alpha /FL=gb:NM_005348.1
218027_at	gb:NM_014175.1 /DEF=Homo sapiens HSPC145 protein (HSPC145), mRNA. /FEA=mrna /GEN=HSPC145 /PROD=HSPC145 protein /DB_XREF=gi:7661805 /UG=Hs.18349 HSPC145 protein /FL=gb:AL136665.1 gb:BC000891.1 gb:AF161494.1 gb:NM_014175.1
217792_at	gb:NM_014426.1 /DEF=Homo sapiens sorting nexin 5 (SNX5), mRNA. /FEA=mrna /GEN=SNX5 /PROD=sorting nexin 5 /DB_XREF=gi:7657598 /UG=Hs.13794 sorting nexin 5 /FL=gb:BC000100.1 gb:AF121855.1 gb:NM_014426.1
221036_s_at	gb:NM_031301.1 /DEF=Homo sapiens hypothetical protein DKFZP564D0372 (DKFZP564D0372), mRNA. /FEA=mrna /GEN=DKFZP564D0372 /PROD=hypothetical protein DKFZP564D0372 /DB_XREF=gi:1375223 /FL=gb:NM_031301.1
201723_s_at	gb:U41514.1 /DEF=Human UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase mRNA, complete cds. /FEA=mrna /PROD=UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase /DB_XREF=gi:1136284 /UG=Hs.80120 UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 1 (GalNAc-T1) /FL=gb:U41514.1 gb:NM_020474.2
202351_at	Consensus includes gb:AI093579 /FEA=EST /DB_XREF=gi:3432555 /DB_XREF=est:q015q06.x1 /CLONE=IMAGE:1696378 /UG=Hs.295726 integrin, alpha V (vitronectin receptor, alpha polypeptide, antigen CD51) /FL=gb:M14648.1 gb:NM_002210.1
208853_s_at	gb:LI18887.1 /DEF=Human calnexin mRNA, complete cds. /FEA=mrna /PROD=calnexin /DB_XREF=gi:306480 /UG=Hs.155560 calnexin /FL=gb:NM_001746.1 gb:BC003552.1 gb:M94859.1 gb:M96452.1 gb:LI0284.1 gb:LI8887.1
213278_at	Consensus includes gb:AW014788 /FEA=EST /DB_XREF=gi:5863545 /DB_XREF=est:UI-H-BIO-aae-h-10-0-UI.s1 /CLONE=IMAGE:2709354 /UG=Hs.48802 Homo sapiens clone 23632 mRNA sequence
203447_at	Consensus includes gb:AU157008 /FEA=EST /DB_XREF=gi:11018529 /DB_XREF=est:AU157008 /CLONE=PLACE1005711 /UG=Hs.193725 proteasome (prosome, macropain) 26S subunit, non-ATPase, 5 /FL=gb:NM_005047.1
212459_x_at	Consensus includes gb:BF593940 /FEA=EST /DB_XREF=gi:11686264 /DB_XREF=est:nab48f10.x1 /CLONE=IMAGE:3269154 /UG=Hs.247309 succinate-CoA ligase, GDP-forming, beta subunit
218514_at	gb:NM_018149.1 /DEF=Homo sapiens hypothetical protein FLJ10587 (FLJ10587), mRNA. /FEA=mrna /GEN=FLJ10587 /PROD=hypothetical protein FLJ10587 /DB_XREF=gi:8922539 /UG=Hs.7296 hypothetical protein FLJ10587 /FL=gb:NM_018149.1
212648_at	Consensus includes gb:AL079292.1 /DEF=Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 48814. /FEA=mrna /PROD=hypothetical protein, similar to (AC007017) putative RNA helicase A Arabidopsis thaliana /DB_XREF=gi:5102732 /UG=Hs.95665 hypothetical protein
200708_at	gb:NM_002080.1 /DEF=Homo sapiens glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2) (GOT2), nuclear gene encoding mitochondrial protein, mRNA. /FEA=mrna /GEN=GOT2 /PROD=aspartate aminotransferase 2 precursor /DB_XREF=gi:4504068 /UG=Hs.170197 glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2) /FL=gb:BC000525.1 gb:M22632.1 gb:NM_002080.1

201064_s_at	gb:NM_003819.2 /DEF=Homo sapiens poly(A)-binding protein, cytoplasmic 4 (inducible form) (PABPC4), mRNA. /FEA=mrna /GEN=PABPC4 /PROD=poly(A)-binding protein, cytoplasmic 4 (inducible form) /DB_XREF=gi:6552335 /UG=Hs.169900 poly(A)-binding protein, cytoplasmic 4 (inducible form) /FL=gb:NM_003819.2
218604_at	gb:NM_014319.2 /DEF=Homo sapiens integral inner nuclear membrane protein (MAN1), mRNA. /FEA=mrna /GEN=MAN1 /PROD=integral inner nuclear membrane protein /DB_XREF=gi:7706606 /UG=Hs.7256 integral inner nuclear membrane protein /FL=gb:AF112299.2 gb:NM_014319.2
214864_s_at	Consensus includes gb:AK024386.1 /DEF=Homo sapiens cDNA FLJ14324 fis, clone FIAC4000100, highly similar to Homo sapiens hydroxyypyruvate reductase (GRHPR) gene. /FEA=mrna /DB_XREF=gi:10436760 /UG=Hs.155742 glyoxylate reductase/hydroxyypyruvate reductase
202717_s_at	gb:NM_003903.1 /DEF=Homo sapiens CDC16 (cell division cycle 16, S. cerevisiae, homolog) (CDC16), mRNA. /FEA=mrna /GEN=CDC16 /PROD=CDC16 (cell division cycle 16, S. cerevisiae, homolog) /DB_XREF=gi:4502700 /UG=Hs.1592 CDC16 (cell division cycle 16, S. cerevisiae, homolog) /FL=gb:NM_003903.1 gb:U18291.1
201643_x_at	gb:NM_016604.1 /DEF=Homo sapiens putative zinc finger protein (LOC51780), mRNA. /FEA=mrna /GEN=LOC51780 /PROD=putative zinc finger protein /DB_XREF=gi:7706598 /UG=Hs.24125 putative zinc finger protein /FL=gb:AF251039.1 gb:NM_016604.1
213803_at	Consensus includes gb:BG545463 /FEA=EST /DB_XREF=EST /DB_XREF=gi:13544128 /DB_XREF=est:602572695F1 /CLONE=IMAGE:4701118 /UG=Hs.180446 karyopherin (importin) beta 1
204689_at	gb:NM_001529.1 /DEF=Homo sapiens hematopoietically expressed homeobox (HHEX), mRNA. /FEA=mrna /GEN=HHEX /PROD=hematopoietically expressed homeobox /DB_XREF=gi:10835016 /UG=Hs.118651 hematopoietically expressed homeobox /FL=gb:NM_001529.1 gb:NM_002729.1
218228_s_at	gb:NM_025235.1 /DEF=Homo sapiens tankyrase 2 (TNKL), mRNA. /FEA=mrna /GEN=TNKL /PROD=tankyrase 2 /DB_XREF=gi:13376841 /UG=Hs.280776 tankyrase 2 /FL=gb:AF264912.1 gb:AF329696.1 gb:NM_025235.1 gb:AF342982.1
202918_s_at	gb:AF151853.1 /DEF=Homo sapiens CGI-95 protein mRNA, complete cds. /FEA=mrna /PROD=CGI-95 protein /DB_XREF=gi:4929658 /UG=Hs.107942
212263_at	DEF2P564M12 protein /FL=gb:AB015441.1 gb:BC005237.1 gb:AF151853.1 gb:AL080070.1 gb:NM_015387.1
212263_at	Consensus includes gb:AI114716 /FEA=EST /DB_XREF=EST /DB_XREF=gi:6360061 /DB_XREF=est:HA1315 /UG=Hs.15020 homolog of mouse quaking QKI (KH domain RNA binding protein) /FL=gb:AF142419.1 gb:AF142422.1
221825_at	Consensus includes gb:AU151793 /FEA=EST /DB_XREF=EST /DB_XREF=gi:11013314 /DB_XREF=est:AU151793 /CLONE=NT2R2006115 /UG=Hs.157078 Homo sapiens cDNA FLJ12793 fis, clone NT2R2002033
211047_x_at	gb:BC006337.1 /DEF=Homo sapiens, clone MGC:12798, mRNA, complete cds. /FEA=mrna /PROD=Unknown (protein for MGC:12798) /DB_XREF=gi:13623468 /FL=gb:BC006337.1
209798_at	gb:DB3243.1 /DEF=Human NPAT mRNA, complete cds. /FEA=mrna /GEN=NPAT /DB_XREF=gi:1304113 /UG=Hs.89385 nuclear protein, ataxia-telangiectasia locus /FL=gb:DB3243.1 gb:NM_002519.1
204361_s_at	gb:AB014486.1 /DEF=Homo sapiens mRNA for RA70, complete cds. /FEA=mrna /GEN=RA70 /PROD=RA70 /DB_XREF=gi:4062959 /UG=Hs.52644 SKAP55 homolog /FL=gb:BC002893.1 gb:AF072166.1 gb:AB014486.1 gb:AF051323.1 gb:NM_003930.1
218127_at	Consensus includes gb:AI804118 /FEA=EST /DB_XREF=gi:5359590 /DB_XREF=est:tc68e01.x1 /CLONE=IMAGE:2069784 /UG=Hs.84928 nuclear transcription factor Y, beta /FL=gb:NM_006166.2 gb:BC005316.1 gb:BC005317.1 gb:U06145.1
220355_s_at	gb:NM_018165.1 /DEF=Homo sapiens hypothetical protein FLJ10645 (FLJ10645), mRNA. /FEA=mrna /GEN=FLJ10645 /PROD=hypothetical protein
202930_s_at	FLJ10645 /DB_XREF=gi:8922564 /UG=Hs.44143 polybromo 1 /FL=gb:AF177387.1 gb:NM_018165.1
202930_s_at	gb:NM_003850.1 /DEF=Homo sapiens succinate-CoA ligase, ADP-forming, beta subunit (SUCL2), mRNA. /FEA=mrna /GEN=SUCL2 /PROD=succinate-CoA ligase, ADP-forming, beta subunit /DB_XREF=gi:1321582 /UG=Hs.182217 succinate-CoA ligase, ADP-forming, beta subunit /FL=gb:NM_003850.1 gb:AB035863.1
203745_at	Consensus includes gb:AI801013 /FEA=EST /DB_XREF=EST /DB_XREF=gi:5366485 /DB_XREF=est:wgl5d09.x1 /CLONE=IMAGE:2365169 /UG=Hs.211571 holocytochrome c synthase (cytochrome c heme-lyase) /FL=gb:U36787.1 gb:NM_005333.1
200597_at	Consensus includes gb:AI123320 /FEA=EST /DB_XREF=EST /DB_XREF=gi:3359086 /DB_XREF=est:qa48a10.x1 /CLONE=IMAGE:1689978 /UG=Hs.198899 eukaryotic translation initiation factor 3, subunit 10 (theta, 150170kD) /FL=gb:U58046.1 gb:U78311.1 gb:NM_003750.1
218519_at	gb:NM_017945.1 /DEF=Homo sapiens hypothetical protein FLJ20730 (FLJ20730), mRNA. /FEA=mrna /GEN=FLJ20730 /PROD=hypothetical protein
203947_at	FLJ20730 /DB_XREF=gi:8923656 /UG=Hs.237480 hypothetical protein FLJ20730 /FL=gb:BC005207.1 gb:NM_017945.1
203947_at	gb:NM_001326.1 /DEF=Homo sapiens cleavage stimulation factor, 3 pre-RNA, subunit 3, 77kD (CSTF3), mRNA. /FEA=mrna /GEN=CSTF3 /PROD=cleavage stimulation factor subunit 3 /DB_XREF=gi:4557494 /UG=Hs.180034 cleavage stimulation factor, 3 pre-RNA, subunit 3, 77kD /FL=gb:NM_001326.1 gb:U15782.1
219002_at	gb:NM_024622.1 /DEF=Homo sapiens hypothetical protein FLJ21901 (FLJ21901), mRNA. /FEA=mrna /GEN=FLJ21901 /PROD=hypothetical protein
220122_at	FLJ21901 /DB_XREF=gi:13375843 /UG=Hs.32646 hypothetical protein FLJ21901 /FL=gb:NM_024622.1
220122_at	gb:NM_024717.1 /DEF=Homo sapiens hypothetical protein FLJ22344 (FLJ22344), mRNA. /FEA=mrna /GEN=FLJ22344 /PROD=hypothetical protein
203882_at	FLJ22344 /DB_XREF=gi:13376020 /UG=Hs.107716 hypothetical protein FLJ22344 /FL=gb:NM_024717.1
203882_at	gb:NM_006084.1 /DEF=Homo sapiens interferon-stimulated transcription factor 3, gamma (48kD) (ISGF3G), mRNA. /FEA=mrna /GEN=ISGF3G /PROD=interferon-stimulated transcription factor 3, gamma (48kD) /DB_XREF=gi:5174474 /UG=Hs.1706 interferon-stimulated transcription factor

212174_at	3, gamma (48kD) /FL-gb:M87503.1 gb:NM_006084.1
202567_at	Consensus includes gb:W02312 /FEA=EST /DB_XREF=gi:1274291 /DB_XREF=est:za08008.r1 /CLONE=IMAGE:291951 /UG=Hs.171811 adenylate kinase 2
218557_at	gb:NM_004175.1 /DEF=Homo sapiens small nuclear ribonucleoprotein D3 polypeptide (18kD) (SNRPD3), mRNA. /FEA=mrna /GEN=SNRPD3 /PROD=small nuclear ribonucleoprotein D3 polypeptide (18kD) /FL-gb:BC000457.1 gb:BC003150.1 gb:NM_004175.1 gb:U15009.1
211976_at	gb:NM_020202.1 /DEF=Homo sapiens Nit protein 2 (NIT2), mRNA. /FEA=mrna /GEN=NIT2 /PROD=Nit protein 2 /DB_XREF=gi:9910459 /UG=Hs.15627 Nit protein 2 /FL-gb:AF260334.1 gb:AF284574.1 gb:NM_020202.1
201990_s_at	Consensus includes gb:AK026168.1 /DEF=Homo sapiens cDNA: FLJ22515 fis, clone HRC12122, highly similar to AF052101 Homo sapiens clone 23872 mRNA sequence. /FEA=mrna /DB_XREF=gi:10438931 /UG=Hs.188882 Homo sapiens cDNA: FLJ21862 fis, clone HEP0321, highly similar to AF052101 Homo sapiens clone 23872 mRNA sequence
208956_x_at	gb:NM_001310.1 /DEF=Homo sapiens cAMP responsive element binding protein-like 2 (CREBL2), mRNA. /FEA=mrna /GEN=CREBL2 /PROD=cAMP responsive element binding protein-like 2 /DB_XREF=gi:4503034 /UG=Hs.13313 cAMP responsive element binding protein-like 2 /FL-gb:AF039081.1
213939_s_at	gb:U62891.1 /DEF=Human deoxyuridine triphosphatase (DUT) mRNA, complete cds. /FEA=mrna /GEN=DUT /PROD=deoxyuridine triphosphatase /DB_XREF=gi:1421817 /UG=Hs.82113 dUTP pyrophosphatase /FL-gb:AB049113.1 gb:U31930.1 gb:U62891.1 gb:NM99913.1 gb:NM_001948.1
201198_s_at	Consensus includes gb:AI871641 /FEA=EST /DB_XREF=gi:5545690 /DB_XREF=est:wg28f04.x1 /CLONE=IMAGE:2342431 /UG=Hs.306623 Homo sapiens cDNA FLJ12012 fis, clone HENBB1001668
203010_at	Consensus includes gb:AI860431 /FEA=EST /DB_XREF=gi:5514047 /DB_XREF=est:w113h07.x1 /CLONE=IMAGE:2424829 /UG=Hs.3887 proteasome (prosome, macropain) 26S subunit, non-ATPase, 1 /FL-gb:D44466.1 gb:NM_002807.1
218067_s_at	gb:NM_003152.1 /DEF=Homo sapiens signal transducer and activator of transcription 5A (STAT5A), mRNA. /FEA=mrna /GEN=STAT5A /PROD=signal transducer and activator of transcription 5A /DB_XREF=gi:4507256 /UG=Hs.167503 signal transducer and activator of transcription 5A /FL-gb:U43185.1 gb:NM_003152.1 gb:U41142.1
219077_s_at	gb:NM_018011.1 /DEF=Homo sapiens hypothetical protein FLJ10154 (FLJ10154), mRNA. /FEA=mrna /GEN=FLJ10154 /PROD=hypothetical protein FLJ10154 /DB_XREF=gi:8922258 /UG=Hs.179972 hypothetical protein FLJ10154 /FL-gb:NM_018011.1
215424_s_at	gb:NM_016373.1 /DEF=Homo sapiens WW domain-containing oxidoreductase (WWOX), mRNA. /FEA=mrna /GEN=WWOX /PROD=FOR II /DB_XREF=gi:7706522 /UG=Hs.519 WW domain-containing oxidoreductase /FL-gb:AF211943.1 gb:NM_016373.1 gb:AF221527.1
219043_s_at	Consensus includes gb:AV689564 /FEA=EST /DB_XREF=gi:10291427 /DB_XREF=est:AV689564 /CLONE=GKCEAA06 /UG=Hs.79008 SKI-INTERACTING PROTEIN
209313_at	gb:NM_024065.1 /DEF=Homo sapiens hypothetical protein MGC3062 (MGC3062), mRNA. /FEA=mrna /GEN=MGC3062 /PROD=hypothetical protein MGC3062 /DB_XREF=gi:13129043 /UG=Hs.94576 hypothetical protein MGC3062 /FL-gb:AF267853.1 gb:BC001021.1 gb:NM_024065.1
202944_at	gb:AB044661.1 /DEF=Homo sapiens XAB1 mRNA for XPA binding protein 1, complete cds. /FEA=mrna /GEN=XAB1 /PROD=XPA binding protein 1 /DB_XREF=gi:11094140 /UG=Hs.18259 XPA binding protein 1; putative ATP (GTP)-binding protein /FL-gb:AB044661.1
209985_s_at	gb:NM_000262.1 /DEF=Homo sapiens N-acetylgalactosaminidase, alpha- (NAGA), mRNA. /FEA=mrna /GEN=NAGA /PROD=alpha-N-acetylgalactosaminidase precursor /DB_XREF=gi:4557780 /UG=Hs.75372 N-acetylgalactosaminidase, alpha- /FL-gb:BC000095.1 gb:M62783.1 gb:M38083.1 gb:NM_000262.1
211656_x_at	gb:BC002719.1 /DEF=Homo sapiens, eukaryotic translation initiation factor 3, subunit 1 (alpha, 35kD), clone MGC3801, mRNA, complete cds. /FEA=mrna /PROD=eukaryotic translation initiation factor 3, subunit 1 (alpha, 35kD) /DB_XREF=gi:12803762 /UG=Hs.173987 eukaryotic translation initiation factor 3, subunit 1 (alpha, 35kD) /FL-gb:BC002719.1 gb:AF090923.1
209358_at	gb:M32577.1 /DEF=Human MHC HLA-DQ beta mRNA, complete cds. /FEA=mrna /GEN=HLA-DQB1 /DB_XREF=gi:188194 /FL-gb:M32577.1
207431_s_at	gb:AF118094.1 /DEF=Homo sapiens PRO2134 mRNA, complete cds. /FEA=mrna /PROD=PRO2134 /DB_XREF=gi:6650833 /UG=Hs.83126 TATA box binding protein (TBP)-associated factor, RNA polymerase II, I. 28kD /FL-gb:D63705.1 gb:NM_005643.1 gb:AF118094.1
213070_at	gb:NM_003676.1 /DEF=Homo sapiens degenerative spermatocyte (homolog Drosophila; lipid desaturase) (DEGS), mRNA. /FEA=mrna /GEN=DEGS /PROD=degenerative spermatocyte /DB_XREF=gi:4505192 /UG=Hs.185973 degenerative spermatocyte (homolog Drosophila; lipid desaturase) /FL-gb:AF002668.1 gb:NM_003676.1
201111_at	Consensus includes gb:AV682436 /FEA=EST /DB_XREF=gi:10284299 /DB_XREF=est:AV682436 /CLONE=GKABE08 /UG=Hs.5848 Homo sapiens mRNA; cDNA DKF2P564L222 (from clone DKF2P564L222)
204370_at	gb:AF053641.1 /DEF=Homo sapiens brain cellular apoptosis susceptibility protein (CSE1) mRNA, complete cds. /FEA=mrna /GEN=CSE1 /PROD=cellular apoptosis susceptibility protein /DB_XREF=gi:3360556 /UG=Hs.90073 chromosome segregation 1 (yeast homolog)-like /FL-gb:AF053641.1 gb:NM_001316.1
	gb:NM_006831.1 /DEF=Homo sapiens ATGCTP-binding protein (HEAB), mRNA. /FEA=mrna /GEN=HEAB /PROD=ATGCTP-binding protein /DB_XREF=gi:5803028 /UG=Hs.87465 ATGCTP-binding protein /FL-gb:BC000446.1 gb:U73524.1 gb:NM_006831.1

202911_at	gb:NM_000179.1 / DEF=Homo sapiens muts (E. coli) homolog 6 (MSH6), mRNA. / FEA=mrna / GEN=MSH6 / PROD=mutS (E. coli) homolog 6 / DB_XREF=gi:4504190 / UG=Hs.3248 mutS (E. coli) homolog 6 / FL=gb:U28946.1 gb:NM_000179.1 gb:U54777.2
204197_s_at	gb:NM_004350.1 / DEF=Homo sapiens runt-related transcription factor 3 (RUNX3), mRNA. / FEA=mrna / GEN=RUNX3 / PROD=runt-related transcription factor 3 / DB_XREF=gi:4757917 / UG=Hs.170019 runt-related transcription factor 3 / FL=gb:NM_004350.1
217809_at	gb:NM_014038.1 / DEF=Homo sapiens HSPC028 protein (HSPC028), mRNA. / FEA=mrna / GEN=HSPC028 / PROD=HSPC028 protein / DB_XREF=gi:7661743 / UG=Hs.5216 HSPC028 protein / FL=gb:AF110323.1 gb:BC003056.1 gb:AF083246.1 gb:NM_014038.1
201054_at	Consensus includes gb:BE966599 / FEA=EST / DB_XREF=gi:11772191 / DB_XREF=est:601660283R1 / CLONE=IMAGE:3906044 / UG=Hs.77492 heterogeneous nuclear ribonucleoprotein A0 / FL=gb:BC001008.1 gb:NM_006805.1 gb:U23803.1
200994_at	Consensus includes gb:BG291787 / FEA=EST / DB_XREF=gi:13050002 / DB_XREF=est:602386007F1 / CLONE=IMAGE:4515240 / UG=Hs.5151 RAN binding protein 7 / FL=gb:AF098799.1 gb:NM_006391.1
201572_x_at	gb:NM_001921.1 / DEF=Homo sapiens dCMP deaminase (DCTD), mRNA. / FEA=mrna / GEN=DCTD / PROD=dCMP deaminase / DB_XREF=gi:4503276 / UG=Hs.76894 dCMP deaminase / FL=gb:U12136.1 gb:NM_001921.1
218195_at	gb:NM_024573.1 / DEF=Homo sapiens hypothetical protein FLJ12910 (FLJ12910), mRNA. / FEA=mrna / GEN=FLJ12910 / PROD=hypothetical protein FLJ12910 / DB_XREF=gi:13375745 / UG=Hs.15929 hypothetical protein FLJ12910 / FL=gb:NM_024573.1
219905_at	gb:NM_018538.1 / DEF=Homo sapiens hypothetical protein PRO2801 (PRO2801), mRNA. / FEA=mrna / GEN=PRO2801 / PROD=hypothetical protein PRO2801 / DB_XREF=gi:8924201 / UG=Hs.181223 hypothetical protein PRO2801 / FL=gb:AF119899.1 gb:NM_018538.1
209362_at	Consensus includes gb:AF688580 / FEA=EST / DB_XREF=gi:4899874 / DB_XREF=est:wg39H05.x1 / CLONE=IMAGE:2330553 / UG=Hs.286145 SRB7 (suppressor of RNA polymerase B, yeast) homolog / FL=gb:U46837.1 gb:U52960.1 gb:NM_004264.1
203983_at	gb:NM_005999.1 / DEF=Homo sapiens translin-associated factor X (TSNAX), mRNA. / FEA=mrna / GEN=TSNAX / PROD=translin-associated factor X / DB_XREF=gi:5174730 / UG=Hs.96247 translin-associated factor X / FL=gb:NM_005999.1
212074_at	Consensus includes gb:BE972774 / FEA=EST / DB_XREF=gi:10586110 / DB_XREF=est:601652004F1 / CLONE=IMAGE:3935281 / UG=Hs.7531 KIAA0810 protein 1 / FL=gb:AF134397.1 gb:NM_013229.1
204859_s_at	gb:NM_013229.1 / DEF=Homo sapiens apoptotic protease activating factor 1 (APAF1), transcript variant 1, mRNA. / FEA=mrna / GEN=APAF1 / PROD=apoptotic protease activating factor isoform a / DB_XREF=gi:7108332 / UG=Hs.77579 apoptotic protease activating factor 1 / FL=gb:AB007873.1 gb:AF134397.1
205707_at	gb:NM_014339.1 / DEF=Homo sapiens interleukin 17 receptor (IL17R), mRNA. / FEA=mrna / GEN=IL17R / PROD=interleukin 17 receptor / DB_XREF=gi:7657229 / UG=Hs.12951 interleukin 17 receptor / FL=gb:U58917.1 gb:NM_014339.1
218716_x_at	gb:NM_012123.1 / DEF=Homo sapiens CGI-02 protein (CGI-02), mRNA. / FEA=mrna / GEN=CGI-02 / PROD=CGI-02 protein / DB_XREF=gi:6912299 / UG=Hs.33979 CGI-02 protein / FL=gb:AF132937.1 gb:NM_012123.1
217940_s_at	gb:NM_018210.1 / DEF=Homo sapiens hypothetical protein FLJ10769 (FLJ10769), mRNA. / FEA=mrna / GEN=FLJ10769 / PROD=hypothetical protein FLJ10769 / DB_XREF=gi:8922653 / UG=Hs.8083 hypothetical protein FLJ10769 / FL=gb:AF151071.1 gb:NM_018210.1
219802_at	gb:NM_024854.1 / DEF=Homo sapiens hypothetical protein FLJ22028 (FLJ22028), mRNA. / FEA=mrna / GEN=FLJ22028 / PROD=hypothetical protein FLJ22028 / DB_XREF=gi:13376278 / UG=Hs.192570 hypothetical protein FLJ22028 / FL=gb:NM_024854.1
209259_s_at	gb:AF020043.1 / DEF=Homo sapiens chromosome-associated polypeptide (HCAP), complete cds. / FEA=mrna / GEN=HCAP / PROD=chromosome-associated polypeptide / DB_XREF=gi:3089367 / UG=Hs.24485 chondroitin sulfate proteoglycan 6 (bamacan) / FL=gb:AF020043.1 gb:NM_005445.1 gb:AF067163.1
212037_at	Consensus includes gb:BF508948 / FEA=EST / DB_XREF=gi:11592146 / DB_XREF=est:U1-H-B14-aor-e-06-0-U1.s1 / CLONE=IMAGE:3085907 / UG=Hs.44499 pinin, desmosome associated protein
211063_s_at	gb:BC006403.1 / DEF=Homo sapiens, NCK adaptor protein 1, clone MGC:12668, mRNA, complete cds. / FEA=mrna / PROD=NCK adaptor protein 1 / DB_XREF=gi:13623576 / FL=gb:BC006403.1
203791_at	gb:NM_005509.2 / DEF=Homo sapiens Dmx-like 1 (DMXL1), mRNA. / FEA=mrna / GEN=DMXL1 / PROD=Dmx-like 1 / DB_XREF=gi:9961348 / UG=Hs.181042 Dmx-like 1 / FL=gb:NM_005509.2
203405_at	gb:NM_003720.1 / DEF=Homo sapiens Down syndrome critical region gene 2 (DSCR2), mRNA. / FEA=mrna / GEN=DSCR2 / PROD=Down syndrome critical region protein 2 / DB_XREF=gi:4505022 / UG=Hs.5198 Down syndrome critical region gene 2 / FL=gb:BC003619.1 gb:NM_003720.1
201604_s_at	gb:NM_002480.1 / DEF=Homo sapiens myosin phosphatase, target subunit 1 (MYPT1), mRNA. / FEA=mrna / GEN=MYPT1 / PROD=myosin phosphatase target subunit 1 / DB_XREF=gi:4505316 / UG=Hs.16533 myosin phosphatase, target subunit 1 / FL=gb:NM_002480.1
218348_s_at	gb:NM_014153.1 / DEF=Homo sapiens HSPC055 protein (HSPC055), mRNA. / FEA=mrna / GEN=HSPC055 / PROD=HSPC055 protein / DB_XREF=gi:7661761 / UG=Hs.179898 HSPC055 protein / FL=gb:AF161540.1 gb:NM_014153.1
203659_at	gb:NM_014707.1 / DEF=Homo sapiens histone deacetylase 7B (HDAC7B-PENDING), mRNA. / FEA=mrna / GEN=HDAC7B-PENDING / PROD=histone deacetylase 7B / DB_XREF=gi:7662279 / UG=Hs.116753 histone deacetylase 7B / FL=gb:AB018287.1 gb:NM_014707.1
202268_s_at	gb:NM_003905.1 / DEF=Homo sapiens amyloid beta precursor protein-binding protein 1, 59KD (APBP1), mRNA. / FEA=mrna / GEN=APBP1 / PROD=amyloid beta precursor protein-binding protein 1, 59KD / DB_XREF=gi:4502168 / UG=Hs.61828 amyloid beta precursor protein-binding protein 1, 59KD

202399_s_at	59KD /FL-gb:AL136798.1 gb:BC000480.1 gb:U0939.1 gb:NM_003905.1
218515_at	gb:NM_005829.1 /DEF=Homo sapiens adaptor-related protein complex 3, sigma 2 subunit (AP3S2), mRNA. /FEA=mrna /GEN=AP3S2 /PROD=adaptor-related protein complex 3, sigma 2 subunit /DB_XREF=gi:5031580 /UG=Hs.154782 adaptor-related protein complex 3, sigma 2 subunit /FL-gb:BC002785.1 gb:NM_005829.1
209180_at	gb:NM_016631.1 /DEF=Homo sapiens hypothetical protein [LOC51325], mRNA. /FEA=mrna /GEN=LOC51325 /PROD=hypothetical protein /DB_XREF=gi:7706175 /UG=Hs.26461 hypothetical protein /FL-gb:AF208862.1 gb:NM_016631.1
205105_at	gb:U49245.1 /DEF=Human geranylgeranyl transferase type II beta-subunit mRNA, complete cds. /FEA=mrna /PROD=geranylgeranyl transferase type II beta-subunit mRNA, complete cds. /FEA=mrna /GEN=MAN2A1 /PROD=mannosidase, alpha, class 2A, member 1 /DB_XREF=gi:4758697 /UG=Hs.32965 mannosidase, alpha, class 2A, member 1 (MAN2A1), mRNA. /FEA=mrna /GEN=MAN2A1 /PROD=mannosidase, alpha, class 2A, member 1 /DB_XREF=gi:1216503 /UG=Hs.78948 Rab geranylgeranyltransferase, beta subunit /FL-gb:U49245.1 gb:NM_004582.1
200666_s_at	gb:NM_006145.1 /DEF=Homo sapiens heat shock 40KD protein 1 (HSPF1), mRNA. /FEA=mrna /GEN=HSPF1 /PROD=heat shock 40KD protein 1 /DB_XREF=gi:5453689 /UG=Hs.82646 DnaJ (Hsp40) homolog, subfamily B, member 1 /FL-gb:BC002352.1 gb:NM_006145.1 gb:D49547.1
200972_at	gb:BC000704.1 /DEF=Homo sapiens, tetraspan 3, clone MGC:965, mRNA, complete cds. /FEA=mrna /PROD=tetraspan 3 /DB_XREF=gi:12653830 /UG=Hs.100090 tetraspan 3 /FL-gb:BC000704.1 gb:BC004280.1 gb:AF054840.1 gb:NM_005724.1 gb:AF133423.1
218352_at	gb:NM_018191.1 /DEF=Homo sapiens hypothetical protein FLJ10716 (FLJ10716), mRNA. /FEA=mrna /GEN=FLJ10716 /PROD=hypothetical protein FLJ10716 /DB_XREF=gi:8922616 /UG=Hs.24129 hypothetical protein FLJ10716 /FL-gb:NM_018191.1
217728_at	gb:NM_014624.2 /DEF=Homo sapiens S100 calcium-binding protein A6 (calyccin) [S100A6], mRNA. /FEA=mrna /GEN=S100A6 /PROD=S100 calcium-binding protein A6 /DB_XREF=gi:9845517 /UG=Hs.275243 S100 calcium-binding protein A6 (calyccin) /FL-gb:BC001431.1 gb:NM_014624.2
211971_s_at	Consensus includes gb:AL653608 /FEA=EST /DB_XREF=gi:4737587 /DB_XREF=est:tz21a06.x1 /CLONE=IMAGE:2289202 /UG=Hs.182490 leucine-rich protein mRNA
212500_at	Consensus includes gb:AL049319.1 /DEF=Homo sapiens mRNA; cDNA DKFZp564C046 (from clone DKFZp564C046). /FEA=mrna /DB_XREF=gi:4500092 /UG=Hs.99821 Homo sapiens mRNA; cDNA DKFZp564C046 (from clone DKFZp564C046)
218473_s_at	gb:NM_024656.1 /DEF=Homo sapiens hypothetical protein FLJ22329 (FLJ22329), mRNA. /FEA=mrna /GEN=FLJ22329 /PROD=hypothetical protein FLJ22329 /DB_XREF=gi:13375904 /UG=Hs.61478 hypothetical protein FLJ22329 /FL-gb:NM_024656.1
203580_s_at	gb:NM_00983.1 /DEF=Homo sapiens solute carrier family 7 (cationic amino acid transporter, y+ system), member 6 (SLC7A6), mRNA. /FEA=mrna /GEN=SLC7A6 /PROD=solute carrier family 7 (cationic amino acid transporter, y+ system), member 6 /FL-gb:D87432.1 gb:NM_003983.1
200900_s_at	carrier family 7 (cationic amino acid transporter, y+ system), member 6 /FL-gb:D87432.1 gb:NM_003983.1
221652_s_at	Consensus includes gb:AF1583537 /FEA=EST /DB_XREF=gi:4569434 /DB_XREF=est:ts12d03.x1 /CLONE=IMAGE:2228357 /UG=Hs.75709 mannose-6-phosphate receptor (cation dependent) /FL-gb:NM_002355.2 gb:M16985.1
217750_s_at	gb:AF274950.1 /DEF=Homo sapiens PNAS-25 mRNA, complete cds. /FEA=mrna /PROD=PNAS-25 /DB_XREF=gi:12751064 /UG=Hs.22595 hypothetical protein FLJ10637 /FL-gb:AF274950.1
203544_s_at	gb:NM_023079.1 /DEF=Homo sapiens hypothetical protein FLJ13855 (FLJ13855), mRNA. /FEA=mrna /GEN=FLJ13855 /PROD=hypothetical protein FLJ13855 /FL-gb:NM_023079.1
221580_s_at	gb:NM_003473.1 /DEF=Homo sapiens signal transducing adaptor molecule (SH3 domain and ITAM motif) 1 (STAM), mRNA. /FEA=mrna /GEN=STAM /PROD=signal transducing adaptor molecule (SH3 domain and ITAM motif) 1 /FL-gb:U43899.1 gb:NM_003473.1
202629_at	gb:BC001972.1 /DEF=Homo sapiens, clone MGC:5306, mRNA, complete cds. /FEA=mrna /PROD=Unknown (protein for MGC:5306) /DB_XREF=gi:12805036 /UG=Hs.301732 hypothetical protein MGC5306 /FL-gb:BC001972.1
205763_s_at	Consensus includes gb:AV681579 /FEA=EST /DB_XREF=gi:10283442 /DB_XREF=est:AV681579 /CLONE=GKAF05 /UG=Hs.84084 amyloid beta precursor protein (cytoplasmic tail)-binding protein 2 /FL-gb:AF017782.1 gb:NM_006380.1
212337_at	gb:NM_006773.2 /DEF=Homo sapiens DEADH (Asp-Glu-Ala-AspHis) box polypeptide 18 (Myc-regulated) (DDX18), mRNA. /FEA=mrna /GEN=DDX18 /PROD=DEADH (Asp-Glu-Ala-AspHis) box polypeptide 18 (Myc-regulated) /FL-gb:NM_006773.2
212244_at	Consensus includes gb:AL687738 /FEA=EST /DB_XREF=gi:4899032 /DB_XREF=est:tp93g08.x1 /CLONE=IMAGE:2206910 /UG=Hs.699 peptidylprolyl isomerase B (cyclophilin B)
222011_s_at	Consensus includes gb:BF224073 /FEA=EST /DB_XREF=gi:11131299 /DB_XREF=est:7q83e05.x1 /CLONE=IMAGE:3704936 /UG=Hs.278544 acetyl-Coenzyme A acetyltransferase 2 (acetoacetyl Coenzyme A thiolase)
204725_s_at	gb:NM_006153.1 /DEF=Homo sapiens NCK adaptor protein 1 (NCK1), mRNA. /FEA=mrna /GEN=NCK1 /PROD=NCK adaptor protein 1 /DB_XREF=gi:5453753 /UG=Hs.54589 NCK adaptor protein 1 /FL-gb:NM_006153.1

208860_s_at	gb:U09820.1 /DEF=Human helicase II (RAD54L) mRNA, complete cds. /FEA=mrna /GEN=RAD54L /PROD=helicase II /DB_XREF=gi:606832 /UG=Hs.96264 alpha thalassemia mental retardation syndrome X-linked (RAD54 (S. cerevisiae) homolog) /FL=gb:U09820.1 gb:NM_000489.1 gb:U72937.2
203224_at	Consensus includes gb:BF340123 /FEA=EST /DB_XREF=gi:11286585 /DB_XREF=est:602037283FL /CLONE=IMAGE:4185212 /UG=Hs.37558 hypothetical prote- in FLJ11149 /FL=gb:NM_018339.1
208619_at	gb:140326.1 /DEF=Homo sapiens Hepatitis B virus X-associated protein 1 mRNA, complete cds. /FEA=mrna /PROD=X-associated protein 1 /DB_XREF=gi:695361 / UG=Hs.108327 damage-specific DNA binding protein 1 (127kd) /FL=gb:U18299.1 gb:NM_001923.2 gb:140326.1
208765_s_at	Consensus includes gb:NM_005826.1 /DEF=Homo sapiens heterogeneous nuclear ribonucleoprotein R (HNRPR), mRNA. /FEA=CDS /GEN=HNRPR /PROD=heterogeneous nuclear ribonucleoprotein R /DB_XREF=gi:5031754 /UG=Hs.15265 heterogeneous nuclear ribonucleoprotein R /FL=gb:BC001449.1 gb:AF000364.1 gb:NM_005826.1
220832_at	gb:NM_016610.1 /DEF=Homo sapiens Toll-like receptor 8 (LOC51311), mRNA. /FEA=mrna /GEN=LOC51311 /PROD=Toll-like receptor 8 /DB_XREF=gi:7706147 / UG=Hs.272410 Toll-like receptor 8 /FL=gb:AF246971.1 gb:NM_016610.1 gb:AF245703.1
208398_s_at	gb:NM_004865.1 /DEF=Homo sapiens TBP-like 1 (TBP1L), mRNA. /FEA=mrna /GEN=TBP1L /PROD=TBP-like 1 /DB_XREF=gi:4759233 /UG=Hs.13993 TBP-like 1 /FL=gb:AF130312.1 gb:NM_004865.1
205077_s_at	gb:NM_002643.1 /DEF=Homo sapiens phosphatidylinositol glycan, class F (PIGF), mRNA. /FEA=mrna /GEN=PIGF /PROD=phosphatidylinositol glycan, class F /DB_XREF=gi:4505796 /UG=Hs.166982 phosphatidylinositol glycan, class F /FL=gb:D13435.1 gb:NM_002643.1
210616_s_at	gb:AB020712.1 /DEF=Homo sapiens mRNA for KIAA0905 protein, complete cds. /FEA=mrna /GEN=KIAA0905 /PROD=KIAA0905 protein /DB_XREF=gi:4240298 /UG=Hs.70266 yeast Sec3lp homolog /FL=gb:AB020712.1
211761_s_at	gb:BC005975.1 /DEF=Homo sapiens, calcyclin binding protein, clone MGC:14660, mRNA, complete cds. /FEA=mrna /PROD=calcyclin binding protein /DB_XREF=gi:13543650 /FL=gb:BC005975.1
213164_at	Consensus includes gb:AI867198 /FEA=EST /DB_XREF=gi:5540214 /DB_XREF=est:wa01c11.x1 /CLONE=IMAGE:2296820 /UG=Hs.324787 solute carrier fam- ily 5 (inositol transporters), member 3 /FL=gb:NM_006933.1
219940_s_at	gb:NM_018386.1 /DEF=Homo sapiens hypothetical protein FLJ11305 (FLJ11305), mRNA. /FEA=mrna /GEN=FLJ11305 /PROD=hypothetical protein FLJ11305 /DB_XREF=gi:8922986 /UG=Hs.7049 hypothetical protein FLJ11305 /FL=gb:NM_018386.1
203800_s_at	Consensus includes gb:BG254653 /FEA=EST /DB_XREF=gi:12764469 /DB_XREF=est:602368621FL /CLONE=IMAGE:4476773 /UG=Hs.247324 hypothetical pro- tein LOC63931 /FL=gb:NM_022100.1
213026_at	Consensus includes gb:BE965998 /FEA=EST /DB_XREF=gi:11770950 /DB_XREF=est:601659892R1 /CLONE=IMAGE:3905710 /UG=Hs.264482 Apg12 (autophagy 12, S. cerevisiae)-like
215165_x_at	Consensus includes gb:AL080099.1 /DEF=Homo sapiens mRNA; cDNA DKFp5564G1272 (from clone DKFp5564G1272); partial cds. /FEA=mrna /GEN=DKFp5564G1272 /PROD=hypothetical protein /DB_XREF=gi:5262522 /UG=Hs.2057 uridine monophosphate synthetase (orotate phosphoribosyl transferase and orotidine-5-decarboxylase)
202864_s_at	gb:NM_003113.1 /DEF=Homo sapiens nuclear antigen Spl00 (SP100), mRNA. /FEA=mrna /GEN=SP100 /PROD=nuclear antigen Spl00 /DB_XREF=gi:4507164 /UG=Hs.77617 nuclear antigen Spl00 /FL=gb:M60618.1 gb:NM_003113.1
208407_s_at	gb:NM_001331.1 /DEF=Homo sapiens catenin (cadherin-associated protein), delta 1 (CTNND1), mRNA. /FEA=mrna /GEN=CTNND1 /PROD=catenin (cadherin-associated protein), delta 1 /DB_XREF=gi:10835009 /UG=Hs.166011 catenin (cadherin-associated protein), delta 1 /FL=gb:NM_001331.1 gb:AF062317.1
202419_at	gb:NM_002035.1 /DEF=Homo sapiens follicular lymphoma variant translocation 1 (FVT1), mRNA. /FEA=mrna /GEN=FVT1 /PROD=follicular lymphoma variant translocation 1 /DB_XREF=gi:4503816 /UG=Hs.74050 follicular lymphoma variant translocation 1 /FL=gb:NM_002035.1
201833_at	gb:NM_001527.1 /DEF=Homo sapiens histone deacetylase 2 (HDAC2), mRNA. /FEA=mrna /GEN=HDAC2 /PROD=histone deacetylase 2 /DB_XREF=gi:4557640 /UG=Hs.3352 histone deacetylase 2 /FL=gb:U31814.1 gb:NM_001527.1
217879_at	Consensus includes gb:AL566824 /FEA=EST /DB_XREF=gi:12919571 /DB_XREF=est:AL566824 /CLONE=CS0DF025YN03 (3 prime) /UG=Hs.172405 cell divi- sion cycle 27 /FL=gb:NM_001256.1

Tabelle 5: Gene aus Clusteranalyse 5

Affymetrix-interne Bezeichnung	Beschreibung der Sequenz in der Genebank Datenbank
201466_s_at	gb:NM_002228.2 /DEF=Homo sapiens v-jun avian sarcoma virus 17 oncogene homolog (JUN), mRNA. /FEA=mrna /GEN=JUN /PROD=v-jun avian sarcoma virus 17 oncogene homolog /DB_XREF=gi:7710122 /UG=Hs.78465 v-jun avian sarcoma virus 17 oncogene homolog /FL=gb:BC002646.1 gb:NM_002228.2
202425_x_at	gb:NM_000944.1 /DEF=Homo sapiens protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform (calcineurin A alpha) (PPP3CA), mRNA. /FEA=mrna /GEN=PPP3CA /PROD=protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform (calcineurin A alpha) /DB_XREF=gi:6715567 /UG=Hs.272458 protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform (calcineurin A alpha) /FL=gb:J05480.1 gb:AL14778.1
218566_s_at	gb:NM_000944.1 gb:AL1353950.1
218566_s_at	gb:NM_012124.1 /DEF=Homo sapiens chord domain-containing protein 1 (CHP1), mRNA. /FEA=mrna /GEN=CHP1 /PROD=chord domain-containing protein 1 /DB_XREF=gi:6912303 /UG=Hs.22857 cysteine and histidine-rich domain (CHORD)-containing, zinc-binding protein 1 /FL=gb:AF192466.1
214349_at	gb:NM_012124.1
204314_s_at	Consensus includes gb:AV764378 /FEA=EST /DB_XREF=gi:10922226 /DB_XREF=est:AV764378 /CLONE=MDSAOE03 /UG=Hs.163863 ESTs, Moderately similar to POL2 HUMAN RETROVIRUS-RELATED POL POLYPROTEIN H. sapiens
208753_s_at	gb:NM_004379.1 /DEF=Homo sapiens CAMP responsive element binding protein 1 (CREB1), mRNA. /FEA=mrna /GEN=CREB1 /PROD=CAMP responsive element binding protein 1 /DB_XREF=gi:4758053 /UG=Hs.79194 CAMP responsive element binding protein 1 /FL=gb:M27691.1 gb:NM_004379.1
215452_x_at	gb:BC002387.1 /DEF=Homo sapiens, nucleosome assembly protein 1-like 1, clone MGC:8688, mRNA, complete cds. /FEA=mrna /PROD=nucleosome assembly protein 1-like 1 /DB_XREF=gi:12803166 /UG=Hs.179662 nucleosome assembly protein 1-like 1 /FL=gb:BC002387.1 gb:AL162068.1
215452_x_at	Consensus includes gb:AL031133 /DEF=Human DNA sequence from clone 281H8 on chromosome 6q25.1-25.3. Contains up to four novel genes, one with similarity to KIAA0323 and worm C30F12.1 and another with Ubiquitin-Like protein gene SMT3 (the latter in an intron of a novel gene). Contains /FEA=mrna_2 /DB_XREF=gi:3676189 /UG=Hs.113293 Human DNA sequence from clone 281H8 on chromosome 6q25.1-25.3. Contains up to four novel genes, one with similarity to KIAA0323 and worm C30F12.1 and another with Ubiquitin-Like protein gene SMT3 (the latter in an intron of a novel gene). Contains ESTs, S
204119_s_at	gb:U90339.1 /DEF=Human adenosine kinase short form mRNA, complete cds. /FEA=mrna /PROD=adenosine kinase short form /DB_XREF=gi:1906010 /UG=Hs.94382 adenosine kinase /FL=gb:U50196.1 gb:BC003568.1 gb:U90339.1 gb:NM_001123.1
201304_at	gb:NM_005000.2 /DEF=Homo sapiens NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 5 (13kD, B13) (NDUFA5), nuclear gene encoding mitochondrial protein, mRNA. /FEA=mrna /GEN=NDUFA5 /PROD=NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 5 /DB_XREF=gi:13699821 /UG=Hs.83916 NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 5 (13kD, B13) /FL=gb:BC000813.1 gb:NM_005000.2 gb:U53468.1 gb:U64028.1
218131_s_at	gb:NM_017660.1 /DEF=Homo sapiens hypothetical protein FLJ20085 (FLJ20085), mRNA. /FEA=mrna /GEN=FLJ20085 /PROD=hypothetical protein FLJ20085 /DB_XREF=gi:8923093 /UG=Hs.118964 hypothetical protein FLJ20085 (FLJ20085) /FL=gb:NM_017660.1
201788_at	gb:NM_007372.1 /DEF=Homo sapiens RNA helicase-related protein (RNAHP), mRNA. /FEA=mrna /GEN=RNAHP /PROD=RNA helicase-related protein /DB_XREF=gi:11321631 /UG=Hs.8765 RNA helicase-related protein /FL=gb:NM_007372.1 gb:AF083255.1
209780_at	gb:AL136883.1 /DEF=Homo sapiens mRNA; cDNA DKFZp434D166 (from clone DKFZp434D166); complete cds. /FEA=mrna /GEN=DKFZp434D166 /PROD=hypothetical protein /DB_XREF=gi:12053266 /UG=Hs.128653 hypothetical protein DKFZp564F013 /FL=gb:AL136883.1
219375_at	gb:NM_006090.1 /DEF=Homo sapiens cholineethanolaminephosphotransferase (CEPT1), mRNA. /FEA=mrna /GEN=CEPT1 /PROD=cholineethanolaminephosphotransferase /DB_XREF=gi:5174414 /UG=Hs.125031 cholineethanolaminephosphotransferase /FL=gb:AF068302.1 gb:NM_006090.1
209181_at	Consensus includes gb:AW516932 /FEA=EST /DB_XREF=gi:7151941 /DB_XREF=est:xq04a05.xl /CLONE=IMAGE:2748848 /UG=Hs.16697 down-regulator of transcription 1, TBP-binding (negative cofactor 2) /FL=gb:BC020809.1
219279_at	gb:NM_017718.1 /DEF=Homo sapiens hypothetical protein FLJ20220 (FLJ20220), mRNA. /FEA=mrna /GEN=FLJ20220 /PROD=hypothetical protein FLJ20220 /DB_XREF=gi:8923209 /UG=Hs.21126 hypothetical protein FLJ20220 /FL=gb:NM_017718.1
206976_s_at	gb:NM_006644.1 /DEF=Homo sapiens heat shock 105kD (HSP105B), mRNA. /FEA=mrna /GEN=HSP105B /PROD=heat shock 105kD /DB_XREF=gi:5729878 /UG=Hs.36927 heat shock 105kD /FL=gb:AB003333.1 gb:NM_006644.1
215596_s_at	Consensus includes gb:AL163248 /DEF=Homo sapiens chromosome 21 segment HS21C048 /FEA=mrna_2 /DB_XREF=gi:7717304 /UG=Hs.288773 zinc finger protein 294
216511_s_at	Consensus includes gb:AJ270770 /DEF=Homo sapiens partial TCF-4 gene for T-cell transcription factor-4, exon 1 and joined CDS features /FEA=mrna_1 /DB_XREF=gi:9188625 /UG=Hs.283857 Homo sapiens partial TCF-4 gene for T-cell transcription factor-4, exon 1 and joined CDS fea-

	tures
201899_at	gb:NM_014888.1 /DEF=Homo sapiens predicted osteoblast protein (GS3786), mRNA. /FEA=mrna /GEN=GS3786 /PROD=predicted osteoblast protein /DB_XREF=gi:7661713 /UG=Hs.29882 predicted osteoblast protein /FL-gb:DB7120.1 gb:NM_014888.1
201435_s_at	Consensus includes gb:AW268640 /FEA=EST /DB_XREF=gi:6655670 /DB_XREF=est:xv52a03.x1 /CLONE=IMAGE:2816716 /UG=Hs.79306 eukaryotic translation initiation factor 4E /FL-gb:M15353.1 gb:NM_001968.1
212232_at	Consensus includes gb:AB023231.1 /DEF=Homo sapiens mRNA for KIAA1014 protein, partial cds. /FEA=mrna /GEN=KIAA1014 /PROD=KIAA1014 protein /DB_XREF=gi:4589677 /UG=Hs.6834 KIAA1014 protein
214329_x_at	Consensus includes gb:AW474434 /FEA=EST /DB_XREF=gi:7044540 /DB_XREF=est:xs95h07.x1 /CLONE=IMAGE:2777437 /UG=Hs.301527 ESTs, Moderately similar to unknown H.sapiens
212099_at	Consensus includes gb:AJ263909 /FEA=EST /DB_XREF=gi:3872112 /DB_XREF=est:qi08f09.x1 /CLONE=IMAGE:1855913 /UG=Hs.204354 ras homolog gene family, member B /FL-gb:NM_004040.1
213618_at	Consensus includes gb:AB011152.1 /DEF=Homo sapiens mRNA for KIAA0580 protein, partial cds. /FEA=mrna /GEN=KIAA0580 /PROD=KIAA0580 protein /DB_XREF=gi:3043683 /UG=Hs.22572 KIAA0580 protein
216899_s_at	Consensus includes gb:AC003999 /DEF=Human PAC clone RP5-1139P1 from 7p15-p21 /FEA=CDS /DB_XREF=gi:2772566 /UG=Hs.52644 SKAP55 homologue
201437_s_at	gb:NM_001968.1 /DEF=Homo sapiens eukaryotic translation initiation factor 4E (EIF4E), mRNA. /FEA=mrna /GEN=EIF4E /PROD=eukaryotic translation initiation factor 4E /DB_XREF=gi:4503534 /UG=Hs.79306 eukaryotic translation initiation factor 4E /FL-gb:M15353.1 gb:NM_001968.1
212122_at	Consensus includes gb:AW771590 /FEA=EST /DB_XREF=gi:7703647 /DB_XREF=est:hm58g08.x1 /CLONE=IMAGE:3032126 /UG=Hs.166982 phosphatidylinositol glycan, class F
208666_s_at	Consensus includes gb:BE866412 /FEA=EST /DB_XREF=gi:10315097 /DB_XREF=est:601678647 /FL-gb:U17714.1 gb:AF116650.1
218252_at	tumorigenicity 13 (colon carcinoma) (Hsp70-Interacting protein) /FL-gb:U17714.1 gb:AF116650.1
	gb:NM_018204.1 /DEF=Homo sapiens cytoskeleton associated protein 2 (CKAP2), mRNA. /FEA=mrna /GEN=CKAP2 /PROD=cytoskeleton associated protein 2
216384_x_at	/DB_XREF=gi:8922641 /UG=Hs.24641 cytoskeleton associated protein 2 /FL-gb:AL136848.1 gb:NM_018204.1
	Consensus includes gb:AF257099 /DEF=Homo sapiens prothymosin alpha (PTMA) gene, complete cds
217100_s_at	sapiens prothymosin alpha (PTMA) gene, complete cds
	Consensus includes gb:AK026451.1 /DEF=Homo sapiens cDNA: FLJ22798 fis, clone KIAA2617. /FEA=mrna /DB_XREF=gi:10439320 /UG=Hs.127287 KIAA0794 protein
204313_s_at	Consensus includes gb:AA161486 /FEA=EST /DB_XREF=gi:1735796 /DB_XREF=est:zq42d09.s1 /CLONE=IMAGE:632369 /UG=Hs.79194 cAMP responsive element binding protein 1 /FL-gb:M27691.1 gb:NM_004379.1
214257_s_at	Consensus includes gb:AA890010 /FEA=EST /DB_XREF=gi:3016889 /DB_XREF=est:aj89h08.s1 /CLONE=IMAGE:1403679 /UG=Hs.50785 SEC22, vesicle trafficking protein (S. cerevisiae)-like 1
218595_s_at	gb:NM_018072.1 /DEF=Homo sapiens hypothetical protein FLJ10359 (FLJ10359), mRNA. /FEA=mrna /GEN=FLJ10359 /PROD=hypothetical protein FLJ10359 /DB_XREF=gi:8922377 /UG=Hs.285861 hypothetical protein FLJ10359 /FL-gb:NM_018072.1
213128_s_at	Consensus includes gb:AA527439 /FEA=EST /DB_XREF=gi:2269568 /DB_XREF=est:ng41f07.s1 /CLONE=IMAGE:937391 /UG=Hs.301667 Homo sapiens mRNA; cDN DKFZp5661043 (from clone DKFZp5661043)
207719_x_at	gb:NM_014812.1 /DEF=Homo sapiens KIAA0470 gene product (KIAA0470), mRNA. /FEA=mrna /GEN=KIAA0470 /PROD=KARP-1-binding protein /DB_XREF=gi:7662141 /UG=Hs.25132 KIAA0470 gene product /FL-gb:AB022657.1 gb:NM_014812.1
200060_s_at	gb:BC001659.1 /DEF=Homo sapiens, RNA-binding protein S1, serine-rich domain, clone MGC:1125, mRNA, complete cds. /FEA=mrna /PROD=RNA-binding protein S1, serine-rich domain /DB_XREF=gi:12804496 /UG=Hs.75104 RNA-binding protein S1, serine-rich domain /FL-gb:BC001659.1 gb:BC001838.1
200634_at	gb:NM_005022.1 /DEF=Homo sapiens profilin 1 (PFN1), mRNA. /FEA=mrna /GEN=PFN1 /PROD=profilin 1 /DB_XREF=gi:4826897 /UG=Hs.75721 profilin 1 /FL-gb:BC002475.1 gb:J03191.1 gb:NM_005022.1
202770_s_at	gb:NM_004354.1 /DEF=Homo sapiens cyclin G2 (CCNG2), mRNA. /FEA=mrna /GEN=CCNG2 /PROD=cyclin G2 /DB_XREF=gi:4757935 /UG=Hs.79069 cyclin G2 /FL-gb:U047414.1 gb:NM_004354.1
201008_s_at	Consensus includes gb:AA812232 /FEA=EST /DB_XREF=gi:2881843 /DB_XREF=est:ob84h09.s1 /CLONE=IMAGE:1338113 /UG=Hs.179526 upregulated by 1,25-dihydroxyvitamin D-3 /FL-gb:NM_006472.1 gb:873591.1
218534_s_at	gb:NM_018046.1 /DEF=Homo sapiens hypothetical protein FLJ10283 (FLJ10283), mRNA. /FEA=mrna /GEN=FLJ10283 /PROD=hypothetical protein FLJ10283 /DB_XREF=gi:8922325 /UG=Hs.284216 hypothetical protein FLJ10283 /FL-gb:NM_018046.1

200993_at	Consensus includes gb:AA939270 /FEA-EST /DB_XREF=gi:3099183 /DB_XREF=est:0q3lb02.sl /CLONE-IMAGE:1587915 /UG-Hs.5151 RAN binding protein 7 / FL-gb:AF098799.1 gb:NM 006391.1
214102_at	Consensus includes gb:AK023737.1 /DEF-Homo sapiens cDNA FLJ13675 f1s, clone PLACE1011875, highly similar to Homo sapiens mRNA for KIAA0580 protein. /FEA-mRNA /DB_XREF=gi:10435758 /UG-Hs.281588 Homo sapiens cDNA FLJ13675 f1s, highly similar to Homo sapiens mRNA for KIAA0580 protein
213704_at	Consensus includes gb:AA129753 /FEA-EST /DB_XREF=gi:1690163 /DB_XREF=est:z116a12.sl /CLONE-IMAGE:502078 /UG-Hs.78948 Rab geranylgeranyltransferase, beta subunit
212367_at	Consensus includes gb:AI799061 /FEA-EST /DB_XREF=gi:5364533 /DB_XREF=est:we98a10.x1 /CLONE-IMAGE:2349114 /UG-Hs.6048 FEM-1 (C.elegans) homolog b /FL-gb:AF178632.1 gb:NM 015322.1 gb:AF204883.1
201873_s_at	gb:NM 002940.1 /DEF-Homo sapiens ATP-binding cassette, sub-family E (ABCE1), mRNA. /FEA-mRNA /GEN=ABCE1 /PROD=ATP-binding cassette, sub-family E, member 1 /DB_XREF=gi:4506558 /UG-Hs.12013 ATP-binding cassette, sub-family E (OABP), member 1 /FL-gb:NM 002940.1
218618_s_at	gb:NM 022763.1 /DEF-Homo sapiens hypothetical protein FLJ23399 (FLJ23399), mRNA. /FEA-mRNA /GEN=FLJ23399 /PROD=hypothetical protein FLJ23399 /DB_XREF=gi:12232434 /UG-Hs.299883 hypothetical protein FLJ23399 /FL-gb:NM 022763.1
203689_s_at	Consensus includes gb:AI743037 /FEA-EST /DB_XREF=gi:5111325 /DB_XREF=est:wq85d05.x1 /CLONE-IMAGE:2371881 /UG-Hs.89764 fragile X mental retardation 1 /FL-gb:NM 002024.1
201074_at	Consensus includes gb:AA593983 /FEA-EST /DB_XREF=gi:2409333 /DB_XREF=est:nml6d01.sl /CLONE-IMAGE:1084033 /UG-Hs.172280 SWISNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 1 /FL-gb:U66615.1 gb:NM 003074.1
200778_s_at	Consensus includes gb:AI191427 /FEA-EST /DB_XREF=gi:3742636 /DB_XREF=est:qe48g03.x1 /CLONE-IMAGE:1742260 /UG-Hs.155595 neural precursor cell expressed, developmentally down-regulated 5 /FL-gb:D28540.1 gb:NM 004404.1 gb:D63878.1
202307_s_at	gb:NM 000593.2 /DEF-Homo sapiens ATP-binding cassette, sub-family B (MDR1AP), member 2 (ABCB2), mRNA. /FEA-mRNA /GEN=ABCB2 /PROD=ATP-binding cassette, sub-family B, member 2 /DB_XREF=gi:9665247 /UG-Hs.158164 ATP-binding cassette, sub-family B (MDR1AP), member 2 /FL-gb:121204.1
213145_at	gb:121205.1 gb:121206.1 gb:121207.1 gb:121208.1 gb:NM 000593.2
218588_s_at	Consensus includes gb:BF001666 /FEA-EST /DB_XREF=gi:10701941 /DB_XREF=est:7g91d12.x1 /CLONE-IMAGE:3313847 /UG-Hs.12460 Homo sapiens clone 23870 mRNA sequence
217834_s_at	gb:NM 018691.1 /DEF-Homo sapiens chromosome 5 open reading frame 3 (C5ORF3), mRNA. /FEA-mRNA /GEN=C5ORF3 /PROD=hypothetical protein /DB_XREF=gi:8922068 /UG-Hs.166551 chromosome 5 open reading frame 3 /FL-gb:NM 018691.1
205038_at	gb:NM 006372.1 /DEF-Homo sapiens NSI-associated protein 1 (NGAP1), mRNA. /FEA-mRNA /GEN=NGAP1 /PROD=NSI-associated protein 1 /DB_XREF=gi:5453805 /UG-Hs.155489 NSI-associated protein 1 /FL-gb:AF155568.1 gb:NM 006372.1
203132_at	Consensus includes gb:BG540504 /FEA-EST /DB_XREF=gi:13532737 /DB_XREF=est:602569230F1 /CLONE-IMAGE:4693783 /UG-Hs.54452 zinc finger protein, subfamily 1A, 1 (Ikaros) /FL-gb:U40462.1 gb:NM 006060.1
211297_s_at	gb:NM 000321.1 /DEF-Homo sapiens retinoblastoma 1 (including osteosarcoma) (RBL), mRNA. /FEA-mRNA /GEN=RBL /PROD=retinoblastoma 1 (including osteosarcoma) /DB_XREF=gi:4506434 /UG-Hs.75770 retinoblastoma 1 (including osteosarcoma) /FL-gb:M33647.1 gb:M15400.1 gb:M28419.1
212375_at	gb:NM 000321.1
208986_at	gb:120320.1 /DEF-Human protein serine/threonine kinase stkl mRNA, complete cds. /FEA-mRNA /PROD=protein serine/threonine kinase /DB_XREF=gi:348242 /UG-Hs.184298 cyclin-dependent kinase 7 (homolog of Xenopus MO15 cdk-activating kinase) /FL-gb:120320.1
217956_s_at	Consensus includes gb:AL563727 /FEA-EST /DB_XREF=gi:12913403 /DB_XREF=est:AL563727 /CLONE-CSODD007Y116 (3 prime) /UG-Hs.306094 trinucleotide repeat containing 12
214870_x_at	Consensus includes gb:AL559478 /FEA-EST /DB_XREF=gi:12905019 /DB_XREF=est:AL559478 /CLONE-CSODJ013Y117 (5 prime) /UG-Hs.21704 transcription factor 12 (HTE4, helix-loop-helix transcription factors 4) /FL-gb:M80627.1 gb:M83233.1 gb:NM 003205.2
209852_x_at	gb:NM 021204.1 /DEF-Homo sapiens E-1 enzyme (MASA), mRNA. /FEA-mRNA /GEN=MASA /PROD=E-1 enzyme /DB_XREF=gi:10864016 /UG-Hs.18442 E-1 enzyme /FL-gb:NM 021204.1 gb:AF113125.1
209063_x_at	Consensus includes gb:AC002045 /DEF-Human Chromosome 16 BAC clone CIT987SK-A-589H1 /FEA-mRNA_2 /DB_XREF=gi:2951945 /UG-Hs.251928 nuclear pore complex interacting protein
201177_s_at	gb:BC001423.1 /DEF-Homo sapiens, Similar to proteasome (prosome, macropain) 28 subunit, 3, clone MGC:1394, mRNA, complete cds. /FEA-mRNA /PROD=Similar to proteasome (prosome, macropain) 28 subunit, 3 /DB_XREF=gi:12655138 /UG-Hs.152978 proteasome (prosome, macropain) activator subunit 3 (PA28 gamma; Ki) /FL-gb:BC001423.1 gb:BC002684.1
212264_s_at	Consensus includes gb:BF248165 /FEA-EST /DB_XREF=gi:11164389 /DB_XREF=est:601859364F1 /CLONE-IMAGE:4069886 /UG-Hs.109643 polyadenylate binding protein-interacting protein 1 /FL-gb:AL136920.1
	gb:NM 005499.1 /DEF-Homo sapiens SUMO-1 activating enzyme subunit 2 (UBA2), mRNA. /FEA-mRNA /GEN=UBA2 /PROD=SUMO-1 activating enzyme subunit 2 /DB_XREF=gi:4885648 /UG-Hs.4311 SUMO-1 activating enzyme subunit 2 /FL-gb:BC003153.1 gb:U35832.1 gb:AF079566.1
	gb:AF110957.1 gb:NM 005499.1 gb:AL136905.1
	Consensus includes gb:BE645850 /FEA-EST /DB_XREF=gi:9970161 /DB_XREF=est:7e77c03.x1 /CLONE-IMAGE:3288484 /UG-Hs.154978 KIAA0261 protein

21218878_s_at	gb:NM_012238.3 / DEF=Homo sapiens sirutin (silent mating type information regulation 2, S. cerevisiae, mRNA. / FEA=mrna / GEN=SIRT1 / PROD=Sir1 / PRO=Sir1) sirutin (silent mating type information regulation 2, S. cerevisiae, homolog) 1 / FL=gb:NM_012238.3 gb:AF083106.2
202163_s_at	gb:NM_004779.1 / DEF=Homo sapiens CCR4-NOT transcription complex, subunit 8 (CNOT8), mRNA. / FEA=mrna / GEN=CNOT8 / PROD=CCR4-NOT transcription complex, subunit 8 / DB_XREF=gi:4758945 / UG=Hs.26703 CCR4-NOT transcription complex, subunit 8 / FL=gb:AF053318.1 gb:NM_004779.1 gb:AL122045.1 gb:AF180476.1
20203584_at	gb:NM_014673.1 / DEF=Homo sapiens KIAA0103 gene product (KIAA0103), mRNA. / FEA=mrna / GEN=KIAA0103 / PROD=KIAA0103 gene product / DB_XREF=gi:7661909 / UG=Hs.154387 KIAA0103 gene product / FL=gb:DL14659.1 gb:NM_014673.1
201901_s_at	Consensus includes gb:Z14077.1 / DEF=H. sapiens mRNA for Y1NF-E1 protein. / FEA=mrna / PROD=Y1 NF-E1 / DB_XREF=gi:38010 / UG=Hs.97496 Y1 transcription factor / FL=gb:MT7698.1 / FL=gb:MT7698.1 gb:MT6541.1 gb:NM_003403.2
21213743_at	Consensus includes gb:BE674119 / FEA=EST / DB_XREF=gi:10034660 / DB_XREF=est:7d75b03.x1 / CLONE=IMAGE:3278765 / UG=Hs.155478 cyclin T2
20202883_s_at	Consensus includes gb:W79584 / FEA=EST / DB_XREF=gi:698093 / DB_XREF=est:ydl71a11.s1 / CLONE=IMAGE:113660 / UG=Hs.108705 protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), beta isoform / FL=gb:NM_002716.1 gb:AF163473.1 gb:AF087438.1
20202069_s_at	Consensus includes gb:A7826060 / FEA=EST / DB_XREF=gi:546731 / DB_XREF=est:wk28a12.x1 / CLONE=IMAGE:2413630 / UG=Hs.250616 isocitrate dehydrogenase 3 (NAD+) alpha / FL=gb:NM_005530.1 gb:U07681.1
21222303_at	Consensus includes gb:AV700891 / FEA=EST / DB_XREF=gi:10302862 / DB_XREF=est:AV700891 / CLONE=GKCBQD03 / UG=Hs.292477 ESTs
20203102_s_at	gb:NM_002408.2 / DEF=Homo sapiens mannosyl (alpha-1,6)-glycoprotein beta-1,2-N-acetylglucosaminyltransferase (MGAT2), mRNA. / FEA=mrna / GEN=MGAT2 / PROD=alpha-1,6-mannosyl-glycoprotein beta-1,2-N-acetylglucosaminyltransferase / DB_XREF=gi:6031183 / UG=Hs.172195 mannosyl (alpha-1,6)-glycoprotein beta-1,2-N-acetylglucosaminyltransferase / FL=gb:NM_002408.2
21212982_at	Consensus includes gb:AF1621223 / FEA=EST / DB_XREF=gi:4630349 / DB_XREF=est:ts77a09.x1 / CLONE=IMAGE:2237272 / UG=Hs.4014 KIAA0946 protein; Huntingtin interacting protein H
20200050_at	gb:NM_007145.1 / DEF=Homo sapiens zinc finger protein 146 (ZNF146), mRNA. / FEA=mrna / GEN=ZNF146 / PROD=zinc finger protein 146 / DB_XREF=gi:6005965 / UG=Hs.301819 zinc finger protein 146 / FL=gb:BC005154.1 gb:NM_007145.1
20202430_s_at	gb:NM_021105.1 / DEF=Homo sapiens phospholipid scramblase 1 (PLSCR1), mRNA. / FEA=mrna / GEN=PLSCR1 / PROD=phospholipid scramblase 1 / DB_XREF=gi:10863876 / UG=Hs.198282 phospholipid scramblase 1 / FL=gb:NM_021105.1 gb:AB006746.1 gb:AF098642.1
21218757_s_at	gb:NM_023010.1 / DEF=Homo sapiens similar to yeast Upf3, variant B (UPF3B), mRNA. / FEA=mrna / GEN=UPF3B / PROD=similar to yeast Upf3, variant B / DB_XREF=gi:12711673 / UG=Hs.103832 similar to yeast Upf3, variant B / FL=gb:AY013251.1 gb:NM_023010.1
21214030_at	Consensus includes gb:BE501352 / FEA=EST / DB_XREF=gi:9703760 / DB_XREF=est:7a1e05.x1 / CLONE=IMAGE:3221312 / UG=Hs.23294 ESTs, weakly similar to T15138 hypothetical protein r28f2.4 - Caenorhabditis elegans C. elegans
21218093_s_at	gb:NM_017664.1 / DEF=Homo sapiens hypothetical protein FLJ20093 (FLJ20093), mRNA. / FEA=mrna / GEN=FLJ20093 / PROD=hypothetical protein FLJ20093 / DB_XREF=gi:8923103 / UG=Hs.172572 hypothetical protein FLJ20093 / FL=gb:NM_017664.1
20203486_s_at	Consensus includes gb:BF195973 / FEA=EST / DB_XREF=gi:11083411 / DB_XREF=est:7088c12.x1 / CLONE=IMAGE:3643391 / UG=Hs.102708 DKFZP434A043 protein / FL=gb:NM_015396.1
2121219303_at	gb:NM_024546.1 / DEF=Homo sapiens hypothetical protein FLJ13449 (FLJ13449), mRNA. / FEA=mrna / GEN=FLJ13449 / PROD=hypothetical protein FLJ13449 / DB_XREF=gi:13375708 / UG=Hs.10711 hypothetical protein FLJ13449 / FL=gb:AL136651.1 gb:NM_024546.1
202173_s_at	gb:NM_007146.1 / DEF=Homo sapiens zinc finger protein 161 (ZNF161), mRNA. / FEA=mrna / GEN=ZNF161 / PROD=zinc finger protein 161 / DB_XREF=gi:6005967 / UG=Hs.6557 zinc finger protein 161 / FL=gb:D28118.1 gb:NM_007146.1
21216903_s_at	Consensus includes gb:AK022697.1 / DEF=Homo sapiens cDNA FLJ12635 fls, clone NT2RM44001865, highly similar to Homo sapiens mRNA for atopy related autoantigen CALC. / FEA=mrna / DB_XREF=gi:10434244 / UG=Hs.61628 calcium binding atopy-related autoantigen 1
20205842_s_at	gb:AF001362.1 / DEF=Homo sapiens Jak2 kinase (JAK2) mRNA, complete cds. / FEA=mrna / GEN=JAK2 / PROD=JAK2 kinase / DB_XREF=gi:3236321 / UG=Hs.115541 Janus kinase 2 (a protein tyrosine kinase) / FL=gb:NM_004972.2 gb:AF005216.1 gb:AF058925.1 gb:AF001362.1
21212702_s_at	Consensus includes gb:M45111 / FEA=EST / DB_XREF=gi:1186277 / DB_XREF=est:y12f12.s1 / CLONE=IMAGE:282863 / UG=Hs.330988 Homo sapiens, similar to Bicucdual D (Drosophila) homolog 1, clone IMAGE:3622452, mRNA, partial cds
20201664_at	gb:AL136877.1 / DEF=Homo sapiens mRNA; cDNA DKFZP434F205 (from clone DKFZP434F205); complete cds. / FEA=mrna / GEN=DKFZP434F205 / PROD=hypothetical protein / DB_XREF=gi:6807670 / UG=Hs.50758 SMC4 (structural maintenance of chromosomes 4, yeast)-like 1 / FL=gb:AB019987.1
20202060_at	gb:NM_005496.1 gb:AL136877.1
20202060_at	gb:NM_014633.1 / DEF=Homo sapiens KIAA0155 gene product (KIAA0155), mRNA. / FEA=mrna / GEN=KIAA0155 / PROD=KIAA0155 gene product / DB_XREF=gi:7661949 / UG=Hs.173288 KIAA0155 gene product / FL=gb:NM_014633.1 gb:D63875.1
20203177_x_at	gb:NM_003201.1 / DEF=Homo sapiens transcription factor 6-like 1 (mitochondrial transcription factor 1-like) (TF6L1), mRNA. / FEA=mrna / GEN=TCF6L1 / PROD=transcription factor 6-like 1 (mitochondrial transcription factor 1-like) / DB_XREF=gi:4507400 / UG=Hs.75133 transcription factor 6-like 1 (mitochondrial transcription factor 1-like) / FL=gb:M62810.1 gb:NM_003201

209748_at	gb:AB029006.1 /DEF-Homo sapiens mRNA for KIAA1083 protein, complete cds. /FEA-mRNA /GEN=KIAA1083 /PROD=KIAA1083 protein /DB_XREF=gi:5689502 /UG=Hs.26334 spastic paraplegia 4 (autosomal dominant; spastin) /FL=gb:AB029006.1
200660_at	gb:NM_005620.1 /DEF-Homo sapiens S100 calcium-binding protein A11 (calgizzarin) (S100A11), mRNA. /FEA-mRNA /GEN=S100A11 /PROD=S100 calcium-binding protein A11 /DB_XREF=gi:5032056 /UG=Hs.256290 S100 calcium-binding protein A11 (calgizzarin) /FL=gb:D49355.1
222119_s_at	gb:BC001410.1 gb:NM_005620.1 gb:D38583.1
208934_s_at	Consensus includes gb:AL117620.1 /DEF-Homo sapiens mRNA; cDNA DKFp564K2364 (from clone DKFp564K2364); partial cds. /FEA-mRNA /GEN=DKFp564K2364 /PROD=hypothetical protein /DB_XREF=gi:5912200 /UG=Hs.284289 vitiligo-associated protein VIT-1
211698_at	gb:AF342815.1 /DEF-Homo sapiens colorectal carcinoma-derived galectin-8 variant 1 mRNA, complete cds. /FEA-mRNA /PROD=colorectal carcinoma-derived galectin-8 variant1 /DB_XREF=gi:13249298 /UG=Hs.4082 lectin, galactoside-binding, soluble, 8 (galectin 8) /FL=gb:AF342815.1 gb:L78132.1 gb:AF074000.1 gb:NM_006499.1
212721_at	gb:AF349444.1 /DEF-Homo sapiens Rb- and p300-binding protein EID-1 mRNA, complete cds. /FEA-mRNA /PROD=Rb- and p300-binding protein EID-1 /DB_XREF=gi:13549113 /FL=gb:AF349444.1
212053_at	Consensus includes gb:AK025504.1 /DEF-Homo sapiens cDNA: FLJ21851 fls, clone HEP01962. /FEA-mRNA /DB_XREF=gi:10438041 /UG=Hs.170218 KIAA0251 protein
209174_s_at	gb:BC000978.2 /DEF-Homo sapiens, hypothetical protein FLJ20259, clone MGC:5396, mRNA, complete cds. /FEA-mRNA /PROD=hypothetical protein FLJ20259 /DB_XREF=gi:12803027 /UG=Hs.9956 hypothetical protein FLJ20259 /FL=gb:BC000978.2 gb:NM_017730.1
203476_at	gb:NM_006670.1 /DEF-Homo sapiens 5T4 oncofetal trophoblast glycoprotein (5T4), mRNA. /FEA-mRNA /GEN=5T4 /PROD=5T4 oncofetal trophoblast glycoprotein /DB_XREF=gi:5729717 /UG=Hs.82128 5T4 oncofetal trophoblast glycoprotein /FL=gb:NM_006670.1
203007_x_at	gb:AF077198.1 /DEF-Homo sapiens lysophospholipase mRNA, complete cds. /FEA-mRNA /PROD=lysophospholipase /DB_XREF=gi:4679009 /UG=Hs.12540 Lysophospholipase I /FL=gb:AF081281.1 gb:AF077198.1 gb:NM_006330.1 gb:AF291053.1
212721_at	Consensus includes gb:AI810380 /FEA-EST /DB_XREF=gi:5396946 /DB_XREF=est:wb87h10.xl /CLONE=IMAGE:2312707 /UG=Hs.47274 Homo sapiens mRNA; cDN DKFp564B176 (from clone DKFp564B176)
218461_at	gb:NM_016301.1 /DEF-Homo sapiens protein x 0004 (LOC51184), mRNA. /FEA-mRNA /GEN=LOC51184 /PROD=protein x 0004 /DB_XREF=gi:9994188 /UG=Hs.284164
214218_s_at	protein x 0004 /FL=gb:AF117229.1 gb:NM_016301.1
218178_s_at	Consensus includes gb:AV699347 /FEA-EST /DB_XREF=gi:10301318 /DB_XREF=est:AV699347 /CLONE=GKCBPH07 /UG=Hs.83623 nuclear receptor subfamily 1 group 1, member 3
217851_s_at	gb:NM_020412.1 /DEF-Homo sapiens CHMP1.5 protein (CHMP1.5), mRNA. /FEA-mRNA /GEN=CHMP1.5 /PROD=CHMP1.5 protein /DB_XREF=gi:9966900 /UG=Hs.42733
202329_at	CHMP1.5 protein /FL=gb:AF281064.1 gb:NM_020412.1
203302_at	gb:NM_016045.1 /DEF-Homo sapiens CGI-107 protein (LOC51012), mRNA. /FEA-mRNA /GEN=LOC51012 /PROD=CGI-107 protein /DB_XREF=gi:7705609 /UG=Hs.3945 CGI-107 protein /FL=gb:AF151865.1 gb:NM_016045.1
201949_x_at	gb:NM_004383.1 /DEF-Homo sapiens c-src tyrosine kinase (CSK), mRNA. /FEA-mRNA /GEN=CSK /PROD=c-src tyrosine kinase /DB_XREF=gi:4758077 /UG=Hs.77793 c-src tyrosine kinase /FL=gb:NM_004383.1
218096_at	gb:NM_000788.1 /DEF-Homo sapiens deoxycytidine kinase (DCK), mRNA. /FEA-mRNA /GEN=DCK /PROD=deoxycytidine kinase /DB_XREF=gi:4503268 /UG=Hs.709 deoxycytidine kinase /FL=gb:M60527.1 gb:NM_000788.1
203255_at	Consensus includes gb:AL572341 /FEA-EST /DB_XREF=gi:12930514 /DB_XREF=est:AL572341 /CLONE=CSODI007YC13 (3 prime) /UG=Hs.76368 capping protel (actin filament) muscle 2-line, beta /FL=gb:NM_004930.1 gb:U03271.1
203855_at	gb:NM_018361.1 /DEF-Homo sapiens hypothetical protein FLJ11210, mRNA. /FEA-mRNA /GEN=FLJ11210 /PROD=hypothetical protein FLJ11210 /DB_XREF=gi:8922941 /UG=Hs.27842 hypothetical protein FLJ11210 /FL=gb:NM_018361.1
218846_at	gb:NM_018693.1 /DEF-Homo sapiens vitiligo-associated protein VIT-1 (VIT1), mRNA. /FEA-mRNA /GEN=VIT1 /PROD=vitiligo-associated protein VIT-1 /DB_XREF=gi:10048403 /UG=Hs.284289 vitiligo-associated protein VIT-1 /FL=gb:NM_018693.1 gb:AF264714.1
208988_at	gb:NM_014969.1 /DEF-Homo sapiens KIAA0893 protein (KIAA0893), mRNA. /FEA-mRNA /GEN=KIAA0893 /PROD=KIAA0893 protein /DB_XREF=gi:7662363 /UG=Hs.3830 KIAA0893 protein /FL=gb:AB020700.1 gb:NM_014969.1
216202_s_at	gb:NM_004830.1 /DEF-Homo sapiens cofactor required for Sp1 transcriptional activation, subunit 3 (130kd) (CRSP3), mRNA. /FEA-mRNA /GEN=CRSP /PROD=cofactor required for Sp1 transcriptional activation, subunit 3 (130kd) /DB_XREF=gi:7019352 /UG=Hs.29679 cofactor required for Sp1 transcriptional activation, subunit 3 (130kd) /FL=gb:AF135022.1 gb:AF105332.1 gb:NM_004830.1
216954_x_at	Consensus includes gb:BE675843 /FEA-EST /DB_XREF=gi:10036384 /DB_XREF=est:7f17b04.xl /CLONE=IMAGE:3294895 /UG=Hs.219614 f-box and leucine-rich repeat protein 11 /FL=gb:AF179221.1
	Consensus includes gb:U15555.1 /DEF-Human serine palmitoyltransferase (LCB2) mRNA, partial cds. /FEA-mRNA /GEN=LCB2 /PROD=serine palmitoyltransferase /DB_XREF=gi:1001944 /UG=Hs.59403 serine palmitoyltransferase, long chain base subunit 2
	Consensus includes gb:877356.1 /DEF-Homo sapiens oligomycin sensitivity conferral protein oscp-like protein mRNA, partial cds. /FEA-mRNA /

	PROD=oligomycin sensitivity conferral protein-like protein / DB_XREF=gi:944964 / UG=Hs.76572 ATP synthase, H ⁺ transporting, mitochondrial F1 complex, O subunit (oligomycin sensitivity conferring protein)
212753_at	Consensus includes gb:AI692203 / FEA=EST / DB_XREF=gi:4969543 / DB_XREF=est:wd37h12.xl / CLONE=IMAGE:2330375 / UG=Hs.8834 ring finger protein 3
207691_x_at	gb:NM_001776.1 / DEF=Homo sapiens ectonucleoside triphosphate diphosphohydrolase 1 (ENTPD1), mRNA. / FEA=mRNA / GEN=ENTPD1 / PROD=ectonucleoside triphosphate diphosphohydrolase1 / DB_XREF=gi:4502666 / UG=Hs.203535 ectonucleoside triphosphate diphosphohydrolase 1 / FL=gb:NM_001776.1
200967_at	gb:NM_000942.1 / DEF=Homo sapiens peptidylprolyl isomerase B (cyclophilin B) (PPIB), mRNA. / FEA=mRNA / GEN=PPIB / PROD=peptidylprolyl isomerase B (cyclophilin B) / DB_XREF=gi:4758949 / UG=Hs.699 peptidylprolyl isomerase B (cyclophilin B) / FL=gb:BC001125.1 gb:M60857.1
201988_s_at	Consensus includes gb:BF438056 / FEA=EST / DB_XREF=gi:11450573 / DB_XREF=est:q66e01.xl / CLONE=IMAGE:3703369 / UG=Hs.13313 cAMP responsive element binding protein-like 2 / FL=gb:AF039081.1 gb:NM_001310.1
202142_at	gb:BC003090.1 / DEF=Homo sapiens, COP9 homolog, clone MGC:1297, mRNA, complete cds. / FEA=mRNA / PROD=COP9 homolog / DB_XREF=gi:13111846 / UG=Hs.75193 COP9 homolog / FL=gb:BC003090.1 gb:U51205.1 gb:NM_006710.1
218238_at	gb:NM_012341.1 / DEF=Homo sapiens GTP-binding protein (NGB), mRNA. / FEA=mRNA / GEN=NGB / PROD=GTP-binding protein / DB_XREF=gi:6912531 / UG=Hs.215766 GTP-binding protein / FL=gb:AF325353.1 gb:AF120334.1 gb:NM_012341.1
205552_s_at	gb:NM_002534.1 / DEF=Homo sapiens 2,5-oligoadenylate synthetase 1 (40-46 kD) (OAS1), transcript variant E16, mRNA. / FEA=mRNA / GEN=OAS1 / PROD=2,5-oligoadenylate synthetase 1, isoform E16 / DB_XREF=gi:8051622 / UG=Hs.82396 2,5-oligoadenylate synthetase 1 (40-46 kD) / FL=gb:BC000562.1
202541_at	gb:D00068.1 gb:NM_002534.1
221699_s_at	Consensus includes gb:BF589679 / FEA=EST / DB_XREF=gi:11682003 / DB_XREF=est:naa08b05.xl / CLONE=IMAGE:3253977 / UG=Hs.146401 small inducible cytokine subfamily E, member 1 (endothelial monocyte-activating) / FL=gb:NM_004757.1 gb:U10117.1
202090_s_at	gb:AF334103.1 / DEF=Homo sapiens nucleolar protein GU2 mRNA, complete cds. / FEA=mRNA / PROD=nucleolar protein GU2 / DB_XREF=gi:13540303 / FL=gb:AF334103.1
202382_s_at	gb:NM_006830.1 / DEF=Homo sapiens ubiquinol-cytochrome c reductase (6.4 kD) subunit (UQCRC), mRNA. / FEA=mRNA / GEN=UQCRC / PROD=ubiquinol-cytochrome c reductase (6.4 kD) subunit / DB_XREF=gi:5803216 / UG=Hs.8372 ubiquinol-cytochrome c reductase (6.4 kD) subunit / FL=gb:DS5636.1 gb:NM_006830.1
220408_x_at	gb:NM_005471.1 / DEF=Homo sapiens glucosamine-6-phosphate isomerase (GNPI), mRNA. / FEA=mRNA / GEN=GNPI / PROD=glucosamine-6-phosphate isomerase / DB_XREF=gi:13027377 / UG=Hs.278500 glucosamine-6-phosphate isomerase / FL=gb:NM_005471.1 gb:AF048826.1 gb:D31766.1
208264_s_at	gb:NM_017569.1 / DEF=Homo sapiens transcription factor (p38 interacting protein) (P38IP), mRNA. / FEA=mRNA / GEN=P38IP / PROD=transcription factor (p38 interacting protein) / DB_XREF=gi:8923734 / UG=Hs.171185 transcription factor (p38 interacting protein) / FL=gb:AF093250.1 gb:NM_017569.1
202872_at	gb:NM_003758.1 / DEF=Homo sapiens eukaryotic translation initiation factor 3, subunit 1 (alpha, 35kD) (EIF3S1), mRNA. / FEA=mRNA / GEN=EIF3S1 / PROD=eukaryotic translation initiation factor 3, subunit 1 (alpha, 35kD) / DB_XREF=gi:4503510 / UG=Hs.173987 eukaryotic translation initiation factor 3, subunit 1 (alpha, 35kD) / FL=gb:U97670.1 gb:NM_003758.1
214935_s_at	Consensus includes gb:AW024925 / FEA=EST / DB_XREF=gi:5878455 / DB_XREF=est:wu92g09.xl / CLONE=IMAGE:2527552 / UG=Hs.86905 ATPase, H ⁺ transporting, lysosomal (vacuolar proton pump) 42kD / FL=gb:NM_001695.1
205263_at	Consensus includes gb:AF131748.1 / DEF=Homo sapiens clone 25191 GTP-specific succinyl-CoA synthetase beta subunit (SCS) mRNA sequence, partial cds. / FEA=mRNA / PROD=GTP-specific succinyl-CoA synthetase beta subunit / DB_XREF=gi:440563 / UG=Hs.247309 succinate-CoA ligase, GDP-forming, beta subunit
218512_at	gb:AF082283.1 / DEF=Homo sapiens CARD-containing apoptotic signaling protein (BCL10) mRNA, complete cds. / FEA=mRNA / GEN=BCL10 / PROD=CARD-containing apoptotic signaling protein / DB_XREF=gi:4092066 / UG=Hs.193516 B-cell CLL/lymphoma 10 / FL=gb:AF082283.1 gb:AF057700.1 gb:AF100338.1 gb:NM_003921.1 gb:AF127386.1 gb:AF134395.1 gb:AF105066.1
210283_x_at	gb:NM_018256.1 / DEF=Homo sapiens hypothetical protein FLJ10881 (FLJ10881), mRNA. / FEA=mRNA / GEN=FLJ10881 / PROD=hypothetical protein FLJ10881 / DB_XREF=gi:8922736 / UG=Hs.73291 hypothetical protein FLJ10881 / FL=gb:AF242546.1 gb:NM_018256.1
202724_s_at	gb:BC005295.1 / DEF=Homo sapiens, similar to polyadenylate binding protein-interacting protein 1, clone NGC:12360, mRNA, complete cds. / FEA=mRNA / PROD=similar to polyadenylate binding protein-interacting protein 1 / DB_XREF=gi:13529010 / UG=Hs.109643 polyadenylate binding protein-interacting protein 1 / FL=gb:BC005295.1
212050_at	gb:NM_002015.2 / DEF=Homo sapiens forkhead box O1A (FOXO1A), mRNA. / FEA=mRNA / GEN=FOXO1A / PROD=forkhead box O1A / DB_XREF=gi:9257221 / UG=Hs.170133 forkhead box O1A (thabdomyosarcoma) / FL=gb:AF032885.1 gb:U02310.1 gb:NM_002015.2
	Consensus includes gb:AI184562 / FEA=EST / DB_XREF=gi:3735200 / DB_XREF=est:qd60b05.xl / CLONE=IMAGE:1733841 / UG=Hs.7976 KIAA0332 protein

212006_at	Consensus includes gb:AU149908 /FEA-EST /DB_XREF=gi:11011429 /DB_XREF=est:AU149908 /CLONE=NT2RP2000896 /UG=Hs.77495 UBX domain-containing 1
222040_at	Consensus includes gb:AI144007 /FEA-EST /DB_XREF=gi:3665816 /DB_XREF=est:qb33c06.x1 /CLONE=IMAGE:1698058 /UG=Hs.249495 heterogenous nuclear ribonucleoprotein A1
202373_s_at	gb:AF255648.1 /DEF=Homo sapiens rGAP-iso mRNA, complete cds. /FEA=mrna /PROD=RGAP-iso /DB_XREF=gi:12005820 /UG=Hs.197289 rab3
209301_at	GTPase-activating protein, non-catalytic subunit (150KD) /FL=gb:AF255648.1 gb:AF004828.1 gb:NM 012414.1
213264_at	gb:M36532.1 /DEF=Human carbonic anhydrase II mRNA, complete cds. /FEA=mrna /GEN=CA2 /DB_XREF=gi:179794 /UG=Hs.155097 carbonic anhydrase II /FL=gb:J03037.1 gb:M36532.1 gb:NM 000067.1
202863_at	Consensus includes gb:AW025150 /FEA-EST /DB_XREF=gi:5878680 /DB_XREF=est:wu94e06.x1 /CLONE=IMAGE:2527714 /UG=Hs.211601 mitogen-activated protein kinase kinase 12
217679_x_at	gb:NM 003113.1 /DEF=Homo sapiens nuclear antigen Sp100 (SP100), mRNA. /FEA=mrna /GEN=SP100 /PROD=nuclear antigen Sp100 /DB_XREF=gi:4507164 /UG=Hs.77617 nuclear antigen Sp100 /FL=gb:M60618.1 gb:NM 003113.1
212802_s_at	Consensus includes gb:AI683552 /FEA-EST /DB_XREF=gi:4893734 /DB_XREF=est:tx67h02.x1 /CLONE=IMAGE:2274675 /UG=Hs.201605 ESTs, Moderately similar to ALU8 HUMAN ALU SUBFAMILY SX SEQUENCE CONTAMINATION WARNING ENTRY H.sapiens
210346_s_at	Consensus includes gb:AK023841.1 /DEF=Homo sapiens cDNA FL13779 fis, clone PLACE4000445, highly similar to Homo sapiens mRNA; cDNA DKF2p434C212 (from clone DKF2p434C212). /FEA=mrna /DB_XREF=gi:10435900 /UG=Hs.172069 DKF2p434C212 protein
208848_at	gb:AF212224.1 /DEF=Homo sapiens CLK4 mRNA, complete cds. /FEA=mrna /PROD=CLK4 /DB_XREF=gi:9437514 /UG=Hs.295231 Homo sapiens CLK4 mRNA, complete cds /FL=gb:AF212224.1
221978_at	gb:M30471.1 /DEF=Human class III alcohol dehydrogenase (ADH5) chi subunit mRNA, complete cds. /FEA=mrna /GEN=ADH5 /PROD=alcohol dehydrogenase 3 /DB_XREF=gi:178133 /UG=Hs.78989 alcohol dehydrogenase 5 (class III), chi polypeptide /FL=gb:NM 000671.2 gb:M29872.1 gb:M30471.1
217526_at	Consensus includes gb:BE136825 /FEA-EST /DB_XREF=gi:8601325 /DB_XREF=est:xw96a07.x1 /CLONE=IMAGE:2835828 /UG=Hs.110309 major histocompatibility complex, class I, F
218322_s_at	Consensus includes gb:AI478300 /FEA-EST /DB_XREF=gi:4371526 /DB_XREF=est:tm39e01.x1 /CLONE=IMAGE:2160504 /UG=Hs.192789 ESTs, Weakly similar to ALU6 HUMAN ALU SUBFAMILY SP SEQUENCE CONTAMINATION WARNING ENTRY H.sapiens
212613_at	gb:NM_016234.2 /DEF=Homo sapiens long-chain fatty acid coenzyme A ligase 5 (FACL5), mRNA. /FEA=mrna /GEN=FACL5 /PROD=long-chain fatty acid coenzyme A ligase 5 /DB_XREF=gi:12669912 /UG=Hs.11638 long-chain fatty acid coenzyme A ligase 5 /FL=gb:NM 016234.2 gb:AB033899.1
204566_at	Consensus includes gb:AI991252 /FEA-EST /DB_XREF=gi:5838157 /DB_XREF=est:wu41e09.x1 /CLONE=IMAGE:2522632 /UG=Hs.87497 butyrophilin, subfamily 3, member A2
	gb:NM 003620.1 /DEF=Homo sapiens protein phosphatase 1D magnesium-dependent, delta isoform (PPM1D), mRNA. /FEA=mrna /GEN=PPM1D /PROD=protein phosphatase 1D magnesium-dependent, delta isoform /DB_XREF=gi:4505996 /UG=Hs.100980 protein phosphatase 1D magnesium-dependent, delta isoform /FL=gb:U78305.1 gb:NM 003620.1

Tabelle 6: Gene aus Clusteranalyse 6

Affymetrix-interne Bezeichnung	Beschreibung der Sequenz in der Genebank Datenbank
202018_s_at	gb:NM_002343.1 / DEF=Homo sapiens lactotransferrin (LTF), mRNA. / FEA=mrna / GEN=LTF / PROD=lactotransferrin / DB_XREF=gi:4505042 / UG=Hs.105938 lactotransferrin / FL=gb:AF332168.1 gb:M33202.1 gb:NM_002343.1
216379_x_at	Consensus includes gb:AK000168.1 / DEF=Homo sapiens cDNA FLJ20161 fis, clone COI09252, highly similar to L33930 Homo sapiens CD24 signal transducer mRNA. / FEA=mrna / DB_XREF=gi:7020079 / UG=Hs.332045 Homo sapiens cDNA FLJ20161 fis, clone COI09252, highly similar to L33930 Homo sapiens CD24 signal transducer mRNA
209771_x_at	Consensus includes gb:AA761181 / FEA=EST / DB_XREF=gi:2810111 / DB_XREF=est:nz09g03.s1 / CLONE-IMAGE:1287316 / UG=Hs.286124 CD24 antigen (small cell lung carcinoma cluster 4 antigen) / FL=gb:X69397.1
206676_at	gb:M33326.1 / DEF=Human nonspecific cross-reacting antigen (NCA) mRNA, complete cds. / FEA=mrna / GEN=NCA / PROD=non-specific cross reacting antigen / B_XREF=gi:189101 / UG=Hs.41 carcinoembryonic antigen-related cell adhesion molecule 8 / FL=gb:M33326.1 gb:NM_001816.1
210254_at	gb:I35848.1 / DEF=Homo sapiens IgE receptor beta chain (HTM4) mRNA, complete cds. / FEA=mrna / GEN=HTM4 / PROD=IgE receptor beta subunit / DB_XREF=gi:561638 / UG=Hs.99960 membrane-spanning 4-domains, subfamily A, member 3 (hematopoietic cell-specific) / FL=gb:NM_006138.1 gb:I35848.1
203887_s_at	gb:NM_000361.1 / DEF=Homo sapiens thrombomodulin (THBD), mRNA. / FEA=mrna / GEN=THBD / PROD=thrombomodulin / DB_XREF=gi:4507482 / UG=Hs.2030 thrombomodulin / FL=gb:M16552.1 gb:NM_000361.1
212768_s_at	Consensus includes gb:AL390736 / DEF=Human DNA sequence from clone RP11-209J19 on chromosome 13 Contains ESTs, STSS and GSSs. Contains the gene for the GW112 protein with two isoforms (GW112 and KIAA4294) / FEA=mrna / DB_XREF=gi:11182238 / UG=Hs.273321 differentially expressed in hematopoietic lineages
202887_s_at	gb:NM_019058.1 / DEF=Homo sapiens hypothetical protein (FLJ20500), mRNA. / FEA=mrna / GEN=FLJ20500 / PROD=hypothetical protein / DB_XREF=gi:9506686 / UG=Hs.111244 hypothetical protein / FL=gb:AL136668.1 gb:NM_019058.1
200916_at	gb:NM_003564.1 / DEF=Homo sapiens transgelin 2 (TAGLN2), mRNA. / FEA=mrna / GEN=TAGLN2 / PROD=transgelin 2 / DB_XREF=gi:4507356 / UG=Hs.75725 transgelin 2 / FL=gb:D21261.1 gb:NM_003564.1
206157_at	gb:NM_002852.1 / DEF=Homo sapiens pentaxin-related gene, rapidly induced by IL-1 beta (PTX3), mRNA. / FEA=mrna / GEN=PTX3 / PROD=pentaxin-related gene, rapidly induced by IL-1 beta / DB_XREF=gi:4506332 / UG=Hs.2050 pentaxin-related gene, rapidly induced by IL-1 beta / FL=gb:M31166.1 gb:NM_002852.1
209369_at	gb:M63310.1 / DEF=Human 1,2-cyclic-inositol-phosphate phosphodiesterase (ANX3) mRNA, complete cds. / FEA=mrna / GEN=ANX3 / PROD=1,2-cyclic-inositol-phosphate phosphodiesterase / DB_XREF=gi:178696 / UG=Hs.1378 annexin A3 / FL=gb:BC000871.1
202497_x_at	gb:M63310.1 gb:M20560.1 gb:NM_005139.1 Consensus includes gb:AI631159 / FEA=EST / DB_XREF=gi:4682489 / DB_XREF=est:ts93405.x1 / CLONE-IMAGE:2238825 / UG=Hs.7594 solute carrier family 2 (facilitated glucose transporter), member 3 / FL=gb:M20681.1 gb:NM_006931.1
205513_at	gb:NM_001062.1 / DEF=Homo sapiens transcobalamin I (vitamin B12 binding protein, R binder family) (TCN1), mRNA. / FEA=mrna / GEN=TCN1 / PROD=transcobalamin I (vitamin B12 binding protein, R binder family) / DB_XREF=gi:4507406 / UG=Hs.2012 transcobalamin I (vitamin B12 binding protein, R binder family) / FL=gb:J05068.1 gb:NM_001062.1
206697_s_at	gb:NM_005143.1 / DEF=Homo sapiens haptoglobin (HP), mRNA. / FEA=mrna / GEN=HP / PROD=haptoglobin / DB_XREF=gi:4826761 / UG=Hs.75990 haptoglobin / FL=gb:K00422.1 gb:L29394.1 gb:NM_005143.1
202146_at	Consensus includes gb:AA747426 / FEA=EST / DB_XREF=gi:2787384 / DB_XREF=est:nx88e08.s1 / CLONE-IMAGE:1269350 / UG=Hs.7879 interferon-related developmental regulator 1 / FL=gb:BC001272.1 gb:NM_001550.1
266_s_at	L33930 / FEATURE= / DEFINITION=HUMCD24B Homo sapiens CD24 signal transducer mRNA, complete cds and 3 region
211657_at	gb:M18728.1 / DEF=Human nonspecific cross-reacting antigen mRNA, complete cds. / FEA=mrna / GEN=NCA; NCA; PROD=non-specific cross reacting antigen / DB_XREF=gi:189084 / FL=gb:M18728.1
205214_at	gb:NM_004226.1 / DEF=Homo sapiens serinethreonine kinase 17b (apoptosis-inducing) (STK17B), mRNA. / FEA=mrna / GEN=STK17B / PROD=serinethreonine kinase 17b (apoptosis-inducing) / DB_XREF=gi:4758193 / UG=Hs.120996 serinethreonine kinase 17b

	(apoptosis-inducing) / FL-gb:AB011421.1 gb:NM_004226.1
207574_s_at	gb:NM_015675.1 / DEF-Homo sapiens growth arrest and DNA-damage-inducible, beta (GADD45B), mRNA. / FEA-mRNA / GEN=GADD45B / PRO=DKEF2P566B133 protein / DB_XREF=gi:9945331 / UG=Hs.110571 growth arrest and DNA-damage-inducible, beta / FL-gb:AF090950.1 gb:NM_015675.1
206343_s_at	gb:NM_013959.1 / DEF-Homo sapiens neuregulin 1 (NRG1), transcript variant SMDP, mRNA. / FEA-mRNA / GEN=NRG1 / PRO=D-neuregulin 1 isoform SMDP // DB_XREF=gi:7669517 / UG=Hs.172816 neuregulin 1 / FL-gb:NM_013959.1 gb:L41827.1
214146_s_at	Consensus includes gb:R64130 / FEA-EST / DB_XREF=gi:836009 / DB_XREF=est:vi18h03.sl / CLONE=IMAGE:139637 / UG=Hs.2164 pro-platelet basic protein (includes platelet basic protein, beta-thromboglobulin, connective tissue-activating peptide III, neutrophil-activating peptide-2)
215716_s_at	Consensus includes gb:L14561 / DEF-Homo sapiens plasma membrane calcium ATPase isoform 1 (ATP2B1) gene, alternative splice products, partial cds / FEA-mRNA 2 / DB_XREF=gi:4165324 / UG=Hs.78546 ATPase, Ca++ transporting, plasma membrane 1
201179_s_at	gb:J03005.1 / DEF-Human alternative guanine nucleotide-binding regulatory protein (G) alpha-inhibitory-subunit mRNA, complete cds. / FEA-mRNA / GEN=GNAL1 / DB_XREF=gi:183183 / UG=Hs.73799 guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 3 / FL-gb:J03005.1 gb:J03198.1 gb:M27543.1 gb:J03238.1 gb:NM_006496.1
201626_at	Consensus includes gb:BG292233 / FEA-EST / DB_XREF=gi:13050848 / DB_XREF=est:602386668F1 / CLONE=IMAGE:4515521 / UG=Hs.56205 insulin induced gene 1 / FL-gb:NM_005542.1
209728_at	gb:BC005312.1 / DEF-Homo sapiens, clone MGC:12387, mRNA, complete cds. / FEA-mRNA / PRO=Unknown (protein for MGC:12387) / DB_XREF=gi:13529035 / UG=Hs.318720 Homo sapiens, clone MGC:12387, mRNA, complete cds / FL-gb:BC005312.1 gb:M16942.1
212665_at	Consensus includes gb:AL556438 / FEA-EST / DB_XREF=gi:12899113 / DB_XREF=est:AL556438 / CLONE=CS0DK004Y118 (3 prime) / UG=Hs.12813 DKFZP4340214 protein
200665_s_at	gb:NM_003118.1 / DEF-Homo sapiens secreted protein, acidic, cysteine-rich (osteonection) (SPARC), mRNA. / FEA-mRNA / GEN=SPARC / PRO=Secreted protein, acidic, cysteine-rich(osteonection) / DB_XREF=gi:4507170 / UG=Hs.111779 secreted protein, acidic, cysteine-rich (osteonection) / FL-gb:BC004974.1 gb:J03040.1 gb:NM_003118.1
201407_s_at	Consensus includes gb:AT186712 / FEA-EST / DB_XREF=gi:3737350 / DB_XREF=est:qe82f01.x1 / CLONE=IMAGE:1745497 / UG=Hs.21537 protein phosphatase 1, catalytic subunit, beta isoform / FL-gb:NM_002709.1 gb:AF092905.1
203505_at	gb:AF285167.1 / DEF-Homo sapiens ATP-binding cassette transporter 1 (ABCA1) mRNA, complete cds. / FEA-mRNA / GEN=ABCA1 / PRO=ATP-binding cassette transporter 1 / DB_XREF=gi:9755158 / UG=Hs.211562 ATP-binding cassette, sub-family A (ABCA1), member 1 / FL-gb:AF165281.1 gb:NM_005502.1 gb:AF285167.1
221802_s_at	Consensus includes gb:AUI57109 / FEA-EST / DB_XREF=gi:11018630 / DB_XREF=est:AUI57109 / CLONE=PLACE1006159 / UG=Hs.23740 KIAA1598 protein
201844_s_at	Consensus includes gb:W84482 / FEA-EST / DB_XREF=gi:1395613 / DB_XREF=est:z489h07.sl / CLONE=IMAGE:356701 / UG=Hs.7910 RING1 and YY1 binding protein / FL-gb:AF179286.1 gb:AB029551.1 gb:NM_012234.1
206390_x_at	gb:NM_002619.1 / DEF-Homo sapiens platelet factor 4 (PF4), mRNA. / FEA-mRNA / GEN=PF4 / PRO=platelet factor 4 / DB_XREF=gi:4505732 / UG=Hs.81564 platelet factor 4 / FL-gb:M25897.1 gb:NM_002619.1
212569_at	Consensus includes gb:AV699744 / FEA-EST / DB_XREF=gi:10301715 / DB_XREF=est:AV699744 / CLONE=GKCRDF05 / UG=Hs.8118 KIAA0650 protein
211960_s_at	Consensus includes gb:BG261416 / FEA-EST / DB_XREF=gi:12771232 / DB_XREF=est:602373192F1 / CLONE=IMAGE:4484422 / UG=Hs.237955 hypothetical protein PQ02706
202422_s_at	gb:NM_022977.1 / DEF-Homo sapiens fatty-acid-Coenzyme A ligase, long-chain 4 (FACL4), transcript variant 2, mRNA. / FEA-mRNA / GEN=FACL4 / PRO=long-chain fatty-acid-Coenzyme A ligase 4, isoform 2 / DB_XREF=gi:12669908 / UG=Hs.81452 fatty-acid-Coenzyme A ligase, long-chain 4 / FL-gb:NM_022977.1
221958_s_at	Consensus includes gb:AA775681 / FEA-EST / DB_XREF=gi:2835015 / DB_XREF=est:zf31a02.sl / CLONE=IMAGE:378506 / UG=Hs.250746 hypothetical protein FLJ23091
204621_s_at	Consensus includes gb:AI935096 / FEA-EST / DB_XREF=gi:5673966 / DB_XREF=est:wp13e10.x1 / CLONE=IMAGE:2464746 / UG=Hs.82120 nuclear receptor subfamily 4, group A, member 2 / FL-gb:NM_006186.1
201409_s_at	gb:NM_002709.1 / DEF-Homo sapiens protein phosphatase 1, catalytic subunit, beta isoform (PPP1CB), mRNA. / FEA-mRNA / GEN=PPP1CB / PRO=protein phosphatase 1, catalytic subunit, beta isoform / DB_XREF=gi:4506004 / UG=Hs.21537 protein phosphatase 1, catalytic subunit, beta isoform / FL-gb:NM_002709.1 gb:AF092905.1
201662_s_at	gb:D89053.1 / DEF-Homo sapiens mRNA for Acyl-CoA synthetase 3, complete cds. / FEA-mRNA / PRO=Acyl-CoA synthetase 3 / DB_XREF=gi:4165017 / UG=Hs.268012 fatty-acid-Coenzyme A ligase, long-chain 3 / FL-gb:NM_004457.2 gb:D89053.1 gb:AF116690.1
220987_s_at	gb:NM_030952.1 / DEF-Homo sapiens hypothetical protein DKFZP434J037 (DKFZP434J037), mRNA. / FEA-mRNA / GEN=DKFZP434J037 / PRO=hypothetical protein DKFZP434J037 / DB_XREF=gi:13569921 / FL-gb:NM_030952.1

219607_s_at	gb:NM_024021.1 /DEF=Homo sapiens membrane-spanning 4-domains, subfamily A, member 4 (MSA4), mRNA. /FEA=mrna /GEN=MSA4 /PROD=membrane-spanning 4-domains, subfamily A, member 4 /DB_XREF=gi:13430865 /UG=Hs.325960 membrane-spanning 4-domains, subfamily A, member 4 /FL=gb:AB013102.1 gb:NM_024021.1 gb:AF068298.1 gb:NM_016650.1
201565_s_at	gb:NM_002166.1 /DEF=Homo sapiens inhibitor of DNA binding 2, dominant negative helix-loop-helix protein (ID2), mRNA. /FEA=mrna /GEN=ID2 /PROD=Inhibitor of DNA binding 2, dominant negative helix-loop-helix protein /DB_XREF=gi:4504570 /UG=Hs.180919 inhibitor of DNA binding 2, dominant negative helix-loop-helix protein /FL=gb:M97796.1 gb:NM_002166.1 gb:D13891.1
213327_s_at	Consensus includes gb:AI820101 /FEA=EST /DB_XREF=gi:5439180 /DB_XREF=est:wq56d12.xl /CLONE=IMAGE:2369111 /UG=Hs.42400 ubiquitin specific protease 12
203603_s_at	gb:NM_014795.1 /DEF=Homo sapiens zinc finger homeobox 1B (ZFHX1B), mRNA. /FEA=mrna /GEN=ZFHX1B /PROD=zinc finger homeobox 1B /DB_XREF=gi:7662183 /UG=Hs.34871 zinc finger homeobox 1B /FL=gb:AB011141.1 gb:NM_014795.1
217963_s_at	gb:NM_014380.1 /DEF=Homo sapiens p75NTR-associated cell death executor; ovarian granulosa cell protein (13kd) (DXS6984E), mRNA. /FEA=mrna /GEN=DXS6984E /PROD=p75NTR-associated cell death executor; ovarian granulosa cell protein (13kd) /DB_XREF=gi:7657043 /UG=Hs.17775 p75NTR-associated cell death executor; ovarian granulosa cell protein (13kd) /EL=gb:NM_014380.1 gb:AF187064.1
206710_s_at	gb:NM_012307.1 /DEF=Homo sapiens differentially expressed in adenocarcinoma of the lung (KIAA0987), mRNA. /FEA=mrna /GEN=KIAA0987 /PROD=KIAA0987 /PROD-differentially expressed in adenocarcinoma of the lung /DB_XREF=gi:6912469 /UG=Hs.103839 erythrocyte membrane protein band 4.1-like 3 /FL=gb:AF069072.1 gb:NM_012307.1
204342_at	gb:NM_013386.1 /DEF=Homo sapiens hypothetical protein (DKFP586G0123), mRNA. /FEA=mrna /GEN=DKFP586G0123 /PROD=hypothetical protein /DB_XREF=gi:9558726 /UG=Hs.24713 hypothetical protein /FL=gb:AL050209.1 gb:NM_013386.1
204393_s_at	gb:NM_001099.2 /DEF=Homo sapiens acid phosphatase, prostate (ACPP), mRNA. /FEA=mrna /GEN=ACPP /PROD=prostatic acid phosphatase precursor /DB_XREF=gi:6382063 /UG=Hs.1852 acid phosphatase, prostate /FL=gb:M24902.1 gb:M34840.1 gb:NM_001099.2
200719_at	Consensus includes gb:BE964043 /FEA=EST /DB_XREF=gi:11767371 /DB_XREF=est:601657616R1 /CLONE=IMAGE:3875955 /UG=Hs.171626 transcription elongation factor B (SIII), polypeptide 1-like /FL=gb:NM_003197.2
202731_at	gb:NM_014456.1 /DEF=Homo sapiens programmed cell death 4 (PDCD4), mRNA. /FEA=mrna /GEN=PDCD4 /PROD=programmed cell death 4 /DB_XREF=gi:7657448 /UG=Hs.296251 programmed cell death 4 /FL=gb:U96628.1 gb:NM_014456.1
204094_s_at	gb:NM_014779.1 /DEF=Homo sapiens KIAA0669 gene product (KIAA0669), mRNA. /FEA=mrna /GEN=KIAA0669 /PROD=KIAA0669 gene product /DB_XREF=gi:7662235 /UG=Hs.52526 KIAA0669 gene product /FL=gb:AB014569.1 gb:NM_014779.1
208690_s_at	gb:BC000915.1 /DEF=Homo sapiens. Similar to LIM protein. Clone MGC:5344, mRNA, complete cds. /FEA=mrna /PROD=Similar to LIM protein /DB_XREF=gi:12654194 /UG=Hs.75807 PDZ and LIM domain 1 (elfin) /FL=gb:BC000915.1
208979_at	gb:AF128458.1 /DEF=Homo sapiens nuclear receptor coactivator RAP250 mRNA, complete cds. /FEA=mrna /PROD=nuclear receptor coactivator RAP250 /DB_XREF=gi:7140573 /UG=Hs.159613 thyroid hormone receptor binding protein /FL=gb:AF177388.1 gb:AF208227.1 gb:AF128458.1 gb:NM_014071.1 gb:AF171667.1 gb:AF245115.1
201772_at	gb:NM_015878.1 /DEF=Homo sapiens antizyme inhibitor (LOC51582), mRNA. /FEA=mrna /GEN=LOC51582 /PROD=antizyme inhibitor /DB_XREF=gi:7706219 /UG=Hs.223014 antizyme inhibitor /FL=gb:D88674.1 gb:NM_015878.1
201345_s_at	gb:NM_003339.1 /DEF=Homo sapiens ubiquitin-conjugating enzyme E2D 2 (homologous to yeast UBC45) (UBE2D2), mRNA. /FEA=mrna /GEN=UBE2D2 /PROD=ubiquitin-conjugating enzyme E2D 2 (homologous to yeast UBC45) /DB_XREF=gi:4507774 /UG=Hs.108332 ubiquitin-conjugating enzyme E2D 2 (homologous to yeast UBC45) /FL=gb:U39317.1 gb:NM_003339.1
221060_s_at	gb:NM_003266.1 /DEF=Homo sapiens toll-like receptor 4 (TLR4), mRNA. /FEA=mrna /GEN=TLR4 /PROD=toll-like receptor 4 /DB_XREF=gi:4507532 /UG=Hs.159239 toll-like receptor 4 /FL=gb:U88880.1 gb:NM_003266.1
208878_s_at	gb:AF032132.1 /DEF=Homo sapiens PAK2 mRNA, complete cds. /FEA=mrna /PROD=PAK2 /DB_XREF=gi:5138913 /UG=Hs.284275 Homo sapiens PAK2 mRNA, 7 complete cds /FL=gb:AF092132.1
212628_at	Consensus includes gb:BG292065 /FEA=EST /DB_XREF=gi:13050507 /DB_XREF=est:602386350F1 /CLONE=IMAGE:4515036 /UG=Hs.69171 protein kinase C-like 2
212928_at	Consensus includes gb:AL050331 /DEF=Human DNA sequence from clone 48613 on chromosome 6q22.1-22.3. Contains the part of a gene for a novel protein, the gene for KIAA0721 (NAP (Nucleosome Assembly Protein) domain containing protein), the TSPYL gene for TSPY-like (testis specific protei... /FEA=mrna_1
221568_s_at	gb:AF090900.1 /DEF=Homo sapiens clone HQ0189 PROO189 mRNA, complete cds. /FEA=mrna /PROD=PROO189 /DB_XREF=gi:568655 /UG=Hs.284141 KIAA0721 protein /FL=gb:NM_021648.1
	gb:AF090900.1 /DEF=Homo sapiens clone HQ0189 PROO189 mRNA, complete cds. /FEA=mrna /PROD=PROO189 /DB_XREF=gi:6690176 /UG=Hs.91393 Homo sapiens cdna: FLJ21887 fls, clone HEPO3135, highly similar to AF090900 Homo sapiens clone HQ0189 PROO189 mRNA /FL=gb:AF090900.1
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202270_at	gb:NM_002053.1 /DEF=Homo sapiens guanylate binding protein 1, interferon-inducible, 67kD (GBP1), mRNA. /FEA=mRNA /GEN=GBP1 /PROD=guanylate binding protein 1, interferon-inducible, 67kD /DB_XREF=gi:4503938
202606_s_at	UG=Hs.62661 guanylate binding protein 1, interferon-inducible, 67kD /FL=gb:BC002666.1 gb:M55542.1 gb:NM_002053.1
202606_s_at	gb:NM_012290.1 /DEF=Homo sapiens tousel-like kinase 1 (TLK1), mRNA. /FEA=mRNA /GEN=TLK1 /PROD=tousel-like kinase 1 /DB_XREF=gi:6912719 /UG=Hs.18895 tousel-like kinase 1 /FL=gb:AF004885.1 gb:NM_012290.1 gb:AF246219.1
216037_x_at	Consensus includes gb:AA664011 /FEA=EST /DB_XREF=gi:2618002 /DB_XREF=est:ac03f10.s1 /CLONE=IMAGE:855403
221561_at	UG=Hs.173638 transcription factor 7- like 2 (T-cell specific, HMG-box)
221561_at	gb:l21934.2 /DEF=Homo sapiens acyl-coenzyme A: cholesterol acyltransferase mRNA, complete cds.
221561_at	/FEA=mRNA /PROD=acyl-coenzyme A: cholesterol acyltransferase /DB_XREF=gi:4878021
203680_at	UG=Hs.14553 sterol O-acyltransferase (acyl-Coenzyme A: cholesterol acyltransferase) 1 /FL=gb:NM_003101.1 gb:l21934.2
203680_at	gb:NM_002736.1 /DEF=Homo sapiens protein kinase, cAMP-dependent, regulatory, type II, beta (PRKAR2B), mRNA.
203680_at	/FEA=mRNA /GEN=PRKAR2B /PROD=protein kinase, cAMP-dependent, regulatory, typeII, beta /DB_XREF=gi:4506064
215111_s_at	UG=Hs.77439 protein kinase, cAMP-dependent, regulatory, type II, beta /FL=gb:M31158.1 gb:NM_002736.1
215111_s_at	Consensus includes gb:AK027071.1 /DEF=Homo sapiens cDNA: FLJ23418 fls, clone HEP21245, highly similar to HSU35048 Human TSC-22 protein mRNA. /FEA=mRNA /DB_XREF=gi:10440100
202211_at	UG=Hs.114360 transforming growth factor beta-stimulated protein TSC-22
202211_at	gb:BC005122.1 /DEF=Homo sapiens, ADP-ribosylation factor GTPase activating protein 1, clone MGC:10272, mRNA, complete cds. /FEA=mRNA /
202211_at	PROD=ADP-ribosylation factor GTPase activatingprotein 1 /DB_XREF=gi:13477296 /UG=Hs.13014 ADP-ribosylation factor GTPase activating protein 1 /FL=gb:BC005122.1 gb:AF111847.1 gb:NM_014570.1
221918_at	Consensus includes gb:AI742210 /FEA=EST /DB_XREF=gi:5110498 /DB_XREF=est:wq39c02.x1 /CLONE=IMAGE:2367458 /UG=Hs.183302 ESTs
213251_at	Consensus includes gb:AV712064 /FEA=EST /DB_XREF=gi:10731370 /DB_XREF=est:AV712064 /CLONE=DCAUD05 /UG=Hs.9456 SWISNF related, matrix associated,
209186_at	actin dependent regulator of chromatin, subfamily a, member 5
209186_at	gb:M23114.1 /DEF=Homo sapiens calcium-ATPase (HK1) mRNA, complete cds. /FEA=mRNA /GEN=HK1 /DB_XREF=gi:184100 /UG=Hs.1526 ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 /FL=gb:M23114.1
210996_s_at	gb:NM_016048.1 /DEF=Human epsilon isoform 14-3-3 protein mRNA, complete cds. /FEA=mRNA /PROD=14-3-3 protein /DB_XREF=gi:4096984 /UG=Hs.79474
210996_s_at	tyrosine 3-monooxygenasetryptophan 5-monooxygenase activation protein, epsilon polypeptide /FL=gb:U43399.1 gb:U43430.1
213624_at	Consensus includes gb:AA873600 /FEA=EST /DB_XREF=gi:2969722 /DB_XREF=est:ob12a02.s1 /CLONE=IMAGE:1323434 /UG=Hs.42945 acid sphingomyelinase-like phosphodiesterase
204634_at	gb:NM_003157.1 /DEF=Homo sapiens serinethreonine kinase 2 (STK2), mRNA. /FEA=mRNA /GEN=STK2 /PROD=serinethreonine kinase 2 /DB_XREF=gi:4507276 /
212515_s_at	UG=Hs.1087 serinethreonine kinase 2 /FL=gb:l20321.1 gb:NM_003157.1
212515_s_at	Consensus includes gb:BG492602 /FEA=EST /DB_XREF=gi:13454114 /DB_XREF=est:602536568F1 /CLONE=IMAGE:4655296 /UG=Hs.147916 DEADH [Asp-Glu-Ala-AspHis] box polypeptide 3
218170_at	gb:NM_016048.1 /DEF=Homo sapiens CGI-111 protein [LOC51015], mRNA. /FEA=mRNA /GEN=LOC51015 /PROD=CGI-111 protein /DB_XREF=gi:7705613 /
218170_at	UG=Hs.11085 CGI-111 protein /FL=gb:AF151869.1 gb:NM_016048.1
210293_s_at	gb:BC005032.1 /DEF=Homo sapiens, Sec23 (S. cerevisiae) homolog B, clone MGC:12666, mRNA, complete cds. /FEA=mRNA /PROD=Sec23 (S. cerevisiae)
221493_at	homolog B /DB_XREF=gi:13477148 /UG=Hs.173497 Sec23 (S. cerevisiae) homolog B /FL=gb:BC005032.1
221493_at	gb:AL1136629.1 /DEF=Homo sapiens mRNA; cDNA DKF2p564D152 (from clone DKF2p564D152); complete cds. /FEA=mRNA /GEN=DKF2p564D152 /
213506_at	PROD=hypothetical protein /DB_XREF=gi:12052783 /UG=Hs.278479 TSPY-like /FL=gb:AL1136629.1
213506_at	Consensus includes gb:BE965369 /FEA=EST /DB_XREF=gi:11769639 /DB_XREF=est:601659282R1 /CLONE=IMAGE:3895653 /UG=Hs.168102 Human proteinase activated receptor-2 mRNA, 3UTR
201016_at	Consensus includes gb:BE542684 /FEA=EST /DB_XREF=gi:9771329 /DB_XREF=est:601067180F1 /CLONE=IMAGE:3453571 /UG=Hs.4310 eukaryotic translation initiation factor 1A /FL=gb:BC000793.1 gb:LI18960.1 gb:NM_001412.1
203414_at	gb:NM_012329.1 /DEF=Homo sapiens monocyte to macrophage differentiation-associated (MMD), mRNA. /FEA=mRNA /GEN=MMD /PROD=monocyte to macrophagedifferentiation-associated, precursor /DB_XREF=gi:6912507 /UG=Hs.79889 monocyte to macrophage differentiation-associated /
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213510_x_at	Consensus includes gb:AW194543 /FEA=EST /DB_XREF=gi:6473381 /DB_XREF=est:xb27c02.x1 /CLONE=IMAGE:2577506 /UG=Hs.234573 Homo sapiens mRNA for
218539_at	TL132 gb:NM 017943.1 /DEF=Homo sapiens hypothetical protein FLJ20725 (FLJ20725), mRNA. /FEA=mrna /GEN=FLJ20725 /PROD=hypothetical protein FLJ20725 /
218172_s_at	DB_XREF=gi:8923650 /UG=Hs.15467 hypothetical protein FLJ20725 (FLJ20725) /FEA=gb:NM 017943.1 gb:NM 018630.1 /DEF=Homo sapiens hypothetical protein PRO2577 (PRO2577), mRNA. /FEA=mrna /GEN=PRO2577 /PROD=hypothetical protein PRO2577 /
202538_s_at	DB_XREF=gi:8924181 /UG=Hs.241576 hypothetical protein PRO2577 (PRO2577) /FEA=gb:AF116708.1 gb:NM 018630.1 gb:NM 014043.1 /DEF=Homo sapiens DKFZP5640123 protein (DKFZP5640123), mRNA. /FEA=mrna /GEN=DKFZP5640123 /PROD=DKFZP5640123 protein /
221504_s_at	DB_XREF=gi:7661633 /UG=Hs.11449 DKFZP5640123 protein (FL=gb:AF151842.1 gb:AL080122.1 gb:NM 014043.1 gb:AF112204.1 /DEF=Homo sapiens Vacuolar proton pump subunit SFD alpha isoform mRNA, complete cds. /FEA=mrna /PROD=Vacuolar proton pump subunit
212213_x_at	SFD alpha isoform /DB_XREF=gi:6563195 /UG=Hs.19575 CGI-11 protein (FL=gb:AF298777.1 gb:AF112204.1 gb:NM 015941.1 Consensus includes gb:AB011139.1 /DEF=Homo sapiens mRNA for KIAA0567 protein, partial cds. /FEA=mrna /GEN=KIAA0567 /PROD=KIAA0567 protein
216632_s_at	DB_XREF=gi:3043657 /UG=Hs.147946 optic atrophy 1 (autosomal dominant) Consensus includes gb:AL137673.1 /DEF=Homo sapiens mRNA; cDNA DKFZp434H0872 (from clone DKFZp434H0872). /FEA=mrna /DB_XREF=gi:6807841 /
221472_at	UG=Hs.306454 Homo sapiens mRNA; cDNA DKFZp434H0872 (from clone DKFZp434H0872) Consensus includes gb:297053 /DEF=Human DNA sequence from clone RPI-179420 on chromosome 20 Contains a 3 end of a novel gene similar to cellular
	retinaldehyde-binding protein, the TDE1 gene (Tumour differentially expressed 1), the PKIG gene encoding protein kinase (cAMP-dependent....
212526_at	FEA=mrna 2 /DB_XREF=gi:9650676 /UG=Hs.272168 tumor differentially expressed 1 /FL=gb:U49188.1 gb:AF112227.1 gb:AF153979.1 gb:NM 006811.1 Consensus includes gb:AK002207.1 /DEF=Homo sapiens cDNA FLJ11345 fis, clone PLACE1010877, highly similar to Homo sapiens mRNA for KIAA0610 protein. /FEA=mrna /DB_XREF=gi:7023938 /UG=Hs.118087 KIAA0610 protein
200624_s_at	Consensus includes gb:AA577695 /FEA=EST /DB_XREF=gi:2355879 /DB_XREF=est:nn2h02.s1 /CLONE=IMAGE:1084659 /UG=Hs.78825 matrin 3 /
201091_s_at	FL=gb:NM 018834.1 gb:AB018266.1 Consensus includes gb:BE748755 /FEA=EST /DB_XREF=gi:10162747 /DB_XREF=est:60157193371 /CLONE=IMAGE:3638737 /UG=Hs.278554 heterochromatin-like
217863_at	protein 1 /FL=gb:AF136630.1 gb:NM 016587.1 Consensus includes gb:AI348378 /FEA=EST /DB_XREF=gi:4085584 /DB_XREF=est:qo20h06.x1 /CLONE=IMAGE:1909115 /UG=Hs.75251 DEADH (Asp-Glu-Ala-AspHis)
202804_at	box binding protein 1 /FL=gb:AF077951.1 gb:AF167160.1 gb:NM 016166.1 Consensus includes gb:AI539710 /FEA=EST /DB_XREF=gi:4453845 /DB_XREF=est:tp77b05.x1 /CLONE=IMAGE:2205297 /UG=Hs.89433 ATP-binding cassette,
214198_s_at	sub-family C (CFTRMRP), member 1 /FL=gb:I05628.1 gb:NM 004996.2 Consensus includes gb:AU150824 /FEA=EST /DB_XREF=gi:11012345 /DB_XREF=est:AU150824 /CLONE=NT2RP2003689 /UG=Hs.2491 DiGeorge syndrome critical
217976_s_at	region gene 2 gb:NM 016141.1 /DEF=Homo sapiens dynein light chain-A (LOC51143), mRNA. /FEA=mrna /GEN=LOC51143 /PROD=dynein light chain-A
202318_s_at	/DB_XREF=gi:7705852 / UG=Hs.266483 dynein light chain-A /FL=gb:AF078849.1 gb:NM 016141.1 gb:AF306508.1 /DEF=Homo sapiens SUMO-1 specific protease FKSG6 mRNA, complete cds. /FEA=mrna /PROD=SUMO-1 specific protease FKSG6 /
208673_s_at	DB_XREF=gi:11096243 /UG=Hs.27197 SUMO-1-specific protease /FL=gb:AF307849.1 gb:AF306508.1 gb:AF196304.1 gb:NM 015571.1 gb:AF107405.1 /DEF=Homo sapiens pre-mRNA splicing factor (SFRS3) mRNA, complete cds. /FEA=mrna /GEN=SFRS3 /PROD=pre-mRNA splicing factor /
218268_at	DB_XREF=gi:5531903 /UG=Hs.167460 splicing factor, arginineserine-rich 3 /FL=gb:BC000914.1 gb:AF107405.1 gb:NM 022771.1 /DEF=Homo sapiens hypothetical protein FLJ12085 (FLJ12085), mRNA. /FEA=mrna /GEN=FLJ12085 /PROD=hypothetical protein FLJ12085 /
209250_at	DB_XREF=gi:12232450 /UG=Hs.48827 hypothetical protein FLJ12085 (FL=gb:NM 022771.1 gb:BC000961.2 /DEF=Homo sapiens, degenerative spermatocyte (homolog Drosophila; lipid desaturase), clone MGC:5079, mRNA, complete cds. /
	FEA=mrna /PROD=degenerative spermatocyte (homolog Drosophila; lipid desaturase) /DB_XREF=gi:12803018 /UG=Hs.185973 degenerative spermatocyte (homolog Drosophila; lipid desaturase) /FL=gb:BC000961.2

218698_at	gb:NM_015957.1 /DEF=Homo sapiens CGI-29 protein (LOC51074), mRNA. /FEA=mRNA /GEN=LOC51074 /PROD=CGI-29 protein /DB_XREF=gi:7705723 /UG=Hs.104058 CGI-29 protein /FL=gb:AF132963.1 gb:NM_015957.1
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Patentansprüche

1. Array bestehend aus Oligo- oder Polynukleotidson-
den, die immobilisiert auf einem festen Träger auf-
gebracht sind, dadurch gekennzeichnet, dass auf der
Oberfläche Sequenzen einer Auswahl oder aller der
in den Tabellen 1-6 genannten selektiven Monozyten-
Makrophagen-Gene gebunden sind.
2. Array nach Anspruch 1, dadurch gekennzeichnet, dass
gegebenenfalls zusätzlich weitere Gene verwendet
werden, von denen bekannt ist, dass sie in jeder
Zelle exprimiert werden und zur Grundausstattung
einer Zelle gehören.
3. Array nach Anspruch 1 und 2, dadurch gekennzeich-
net, dass mit den genannten Genen komplementäre RNA
auf der Oberfläche des Arrays gebunden ist zum in-
versen Nachweis über die in den Tabellen 1-6 darge-
stellten Gene oder Gensequenzen.
4. Array nach Anspruch 1 bis 3, dadurch gekennzeich-
net, dass die Gene, deren Teil- und Oligomersequen-
zen krankheits- und nebenwirkungsrelevante selekti-
onierte Gene der rheumatoiden Arthritis oder ande-
rer chronisch entzündlichen Erkrankungen vor und
nach anti-TNF-Therapie sind.
5. Array nach Anspruch 1 bis 4, dadurch gekennzeich-
net, dass die Gene, deren Teilsequenzen und Oligo-
mersequenzen krankheitsspezifisch regulierte Gene
des Monozyten/Makrophagen-Zellsystems sind.

6. Array nach Anspruch 1 bis 5, dadurch gekennzeichnet, dass auf der Oberfläche gegebenenfalls auch Allele, Derivate und/oder Splicingvarianten der Gen- bzw. Genteilsequenzen und Oligomersequenzen vorliegen.
- 5
7. Array nach Anspruch 1 bis 6, dadurch gekennzeichnet, dass es auf der Oberfläche Gensequenzen enthält, die mindestens eine Teil-Sequenzidentität von 80 % in den Protein-kodierenden Abschnitten der mRNA besitzen.
- 10
8. Array nach Anspruch 1 bis 7, dadurch gekennzeichnet, dass die Oberfläche der Träger mit reaktiven Gruppen, Metallverbindungen oder Legierungen beschichtet ist.
- 15
9. Array nach Anspruch 1 bis 8, dadurch gekennzeichnet, dass die Gene oder Gensequenzen durch Spottingverfahren von cDNA, Immobilisierungsverfahren und Syntheseverfahren von Oligomeren oder spiegelbildlich in Form von RNA aufgebracht sind.
- 20
10. Verwendung des Arrays nach Anspruch 1 bis 9 mit Proben, die zum Nachweis Fluoreszenzfarbstoff-, Enzym-, Protein- oder radioaktiv markiert sind und eine Verstärkung zulassen.
- 25
11. Verwendung des Arrays nach Anspruch 1 bis 9 mit Proben, dadurch gekennzeichnet, dass die Verstärkung der Signale über gekoppelte alkalische Phosphatase, Peroxidase, Biotin Digoxigenin-, Proteinmoleküle, (Edel-)Metallchelate oder Beads erfolgt.
- 30

12. Verwendung des Arrays nach Anspruch 1 bis 9 mit Proben, dadurch gekennzeichnet, dass zur zusätzlichen Verstärkung der Signale Streptavidin, (Edel-)Metallchelate, Beads oder Antikörper eingesetzt werden.
- 5
13. Verwendung des Arrays nach Anspruch 1 bis 9 zum inversen Nachweis festphasengebundener Total-RNA oder messenger-RNA.
- 10
14. Verwendung des Arrays nach Anspruch 1 bis 9 zur Messung der Monozyten/Makrophagen-Aktivierung oder der Entzündungsaktivität im Blut oder im Zellgewebe.
- 15
15. Verwendung des Arrays nach Anspruch 1 bis 9 zur Feindiagnostik sowie zur Früherkennung von entzündlichen Erkrankungen und der rheumatoiden Arthritis.
- 20
16. Verwendung des Arrays nach Anspruch 1 bis 9 zur Verfolgung von Nebenwirkungen bei der anti-TNF-Therapie von entzündlichen Erkrankungen und der rheumatoiden Arthritis.
- 25
17. Verwendung des Arrays nach Anspruch 1 bis 9 zur Überwachung der Therapie und Erstellung einer Prognose bei entzündlichen Erkrankungen und der rheumatoiden Arthritis.
- 30
18. Verwendung der Arrays nach Anspruch 1 bis 9 zur Identifizierung von pharmazeutischen Targets bei entzündlichen Erkrankungen und der rheumatoiden Arthritis.

19. Verwendung der Gene oder Gensequenzen nach Tabelle 1-6 zu Einzelgennachweisverfahren, vorzugsweise reverse Transkriptions-PCR (RT-PCR).
- 5 20. Verwendung der Gene oder Gensequenzen nach Tabelle 1-6, dadurch gekennzeichnet, dass sie mit einer Markierung oder einer Reporterfunktion ausgestattet sind.
- 10 21. Verwendung der Gene oder Gensequenzen nach Tabelle 1-6 zum reversen Nachweis festphasengebundener Total-RNA oder messenger-RNA in einem RNA-Array mit bis zu 500 Gewebs- und/oder Blutproben.

INTERNATIONAL SEARCH REPORT

International Application No

P 03/01822

A. CLASSIFICATION OF SUBJECT MATTER
IPC 7 C12Q1/68

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
IPC 7 C12Q

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

EPO-Internal, BIOSIS, EMBASE, Sequence Search

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category °	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	STUHLMÜLLER ET AL.: "Identification of known and novel genes in activated monocytes from patients with rheumatoid arthritis" ARTHRITIS & RHEUMATISM, vol. 43, no. 4, April 2000 (2000-04), pages 775-790, XP002255228 the whole document	
A	HELLER R A ET AL: "Discovery and analysis of inflammatory disease-related genes using cDNA microarrays" PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF USA, NATIONAL ACADEMY OF SCIENCE. WASHINGTON, US, no. 94, pages 2150-2155, XP002076789 ISSN: 0027-8424 the whole document	

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Further documents are listed in the continuation of box C.



Patent family members are listed in annex.

° Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier document but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"&" document member of the same patent family

Date of the actual completion of the international search

23 September 2003

Date of mailing of the international search report

27.01.2004

Name and mailing address of the ISA

European Patent Office, P.B. 5818 Patentlaan 2
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Authorized officer

Bort, S

INTERNATIONAL SEARCH REPORT

International Application No

P. DE 03/01822

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category °	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	<p>SMEETS ET AL.: "Quantitative analysis of chemokine expression in rheumatoid synovial tissue after treatment with anti-TNF and IFN-beta" ARTHRITIS AND RHEUMATISM, vol. 42, no. 9, September 1999 (1999-09), page s93, XP008022391 abstract</p> <p>-----</p>	
A	<p>DATABASE EBI [Online] 7 January 1995 (1995-01-07), TRUCCO: "Human MHC clas II DG-beta associated with DRw6, DQw1 protein, complete cds." XP002255230 Database accession no. M17565</p> <p>-----</p>	

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

See continuation sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

1-21 (all in part)

4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
☐ No protest accompanied the payment of additional search fees.

OTHER INFORMATION**PCT/ISA/ 210**

The International Searching Authority has determined that this international application contains multiple (groups of) inventions, namely

1. Claims 1-21 (all in part)

Inventions 1-1500

array consisting of at least one of the genes specified in tables 1-6, and use of the array,

where the gene bank accession numbers corresponding to gene sequence are:

- for Invention 1: M17565.1

- for Invention 2: X00452.1

- for Inventions 3-1500: BF338947-NM_015957.1

A. KLASSIFIZIERUNG DES ANMELDUNGSGEGENSTANDES

IPK 7 C12Q1/68

Nach der Internationalen Patentklassifikation (IPK) oder nach der nationalen Klassifikation und der IPK

B. RECHERCHIERTE GEBIETE

Recherchierte Mindestprüfstoff (Klassifikationssystem und Klassifikationssymbole)

IPK 7 C12Q

Recherchierte aber nicht zum Mindestprüfstoff gehörende Veröffentlichungen, soweit diese unter die recherchierten Gebiete fallen

Während der internationalen Recherche konsultierte elektronische Datenbank (Name der Datenbank und evtl. verwendete Suchbegriffe)

EPO-Internal, BIOSIS, EMBASE, Sequence Search

C. ALS WESENTLICH ANGESEHENE UNTERLAGEN

Kategorie*	Bezeichnung der Veröffentlichung, soweit erforderlich unter Angabe der in Betracht kommenden Teile	Betr. Anspruch Nr.
A	STUHLMÜLLER ET AL.: "Identification of known and novel genes in activated monocytes from patients with rheumatoid arthritis" ARTHRITIS & RHEUMATISM, Bd. 43, Nr. 4, April 2000 (2000-04), Seiten 775-790, XP002255228 das ganze Dokument	
A	HELLER R A ET AL: "Discovery and analysis of inflammatory disease-related genes using cDNA microarrays" PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF USA, NATIONAL ACADEMY OF SCIENCE. WASHINGTON, US, Nr. 94, Seiten 2150-2155, XP002076789 ISSN: 0027-8424 das ganze Dokument	



Weitere Veröffentlichungen sind der Fortsetzung von Feld C zu entnehmen



Siehe Anhang Patentfamilie

* Besondere Kategorien von angegebenen Veröffentlichungen :

"A" Veröffentlichung, die den allgemeinen Stand der Technik definiert, aber nicht als besonders bedeutsam anzusehen ist

"E" älteres Dokument, das jedoch erst am oder nach dem internationalen Anmeldedatum veröffentlicht worden ist

"L" Veröffentlichung, die geeignet ist, einen Prioritätsanspruch zweifelhaft erscheinen zu lassen, oder durch die das Veröffentlichungsdatum einer anderen im Recherchenbericht genannten Veröffentlichung belegt werden soll oder die aus einem anderen besonderen Grund angegeben ist (wie ausgeführt)

"O" Veröffentlichung, die sich auf eine mündliche Offenbarung, eine Benutzung, eine Ausstellung oder andere Maßnahmen bezieht

"P" Veröffentlichung, die vor dem internationalen Anmeldedatum, aber nach dem beanspruchten Prioritätsdatum veröffentlicht worden ist

"T" Spätere Veröffentlichung, die nach dem internationalen Anmeldedatum oder dem Prioritätsdatum veröffentlicht worden ist und mit der Anmeldung nicht kollidiert, sondern nur zum Verständnis des der Erfindung zugrundeliegenden Prinzips oder der ihr zugrundeliegenden Theorie angegeben ist

"X" Veröffentlichung von besonderer Bedeutung; die beanspruchte Erfindung kann allein aufgrund dieser Veröffentlichung nicht als neu oder auf erfinderischer Tätigkeit beruhend betrachtet werden

"Y" Veröffentlichung von besonderer Bedeutung; die beanspruchte Erfindung kann nicht als auf erfinderischer Tätigkeit beruhend betrachtet werden, wenn die Veröffentlichung mit einer oder mehreren anderen Veröffentlichungen dieser Kategorie in Verbindung gebracht wird und diese Verbindung für einen Fachmann naheliegend ist

"&" Veröffentlichung, die Mitglied derselben Patentfamilie ist

Datum des Abschlusses der internationalen Recherche

23. September 2003

Absendedatum des internationalen Recherchenberichts

27. 01. 2004

Name und Postanschrift der Internationalen Recherchenbehörde

Europäisches Patentamt, P.B. 5818 Patentlaan 2
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Tel. (+31-70) 340-2040, Tx. 31 651 epo nl,
Fax: (+31-70) 340-3016

Bevollmächtigter Bediensteter

Bort, S

C.(Fortsetzung) ALS WESENTLICH ANGESEHENE UNTERLAGEN		
Kategorie	Bezeichnung der Veröffentlichung, soweit erforderlich unter Angabe der in Betracht kommenden Teile	Betr. Anspruch Nr.
A	<p>SMEETS ET AL.: "Quantitative analysis of chemokine expression in rheumatoid synovial tissue after treatment with anti-TNF and IFN-beta" ARTHRITIS AND RHEUMATISM, Bd. 42, Nr. 9, September 1999 (1999-09), Seite s93, XP008022391 Zusammenfassung</p> <p>-----</p>	
A	<p>DATABASE EBI [Online] 7. Januar 1995 (1995-01-07), TRUCCO: "Human MHC class II DG-beta associated with DRw6, DQw1 protein, complete cds." XP002255230 Database accession no. M17565</p> <p>-----</p>	

Feld I Bemerkungen zu den Ansprüchen, die sich als nicht recherchierbar erwiesen haben (Fortsetzung von Punkt 2 auf Blatt 1)

Gemäß Artikel 17(2)a) wurde aus folgenden Gründen für bestimmte Ansprüche kein Recherchenbericht erstellt:

1. ☐ Ansprüche Nr.
weil sie sich auf Gegenstände beziehen, zu deren Recherche die Behörde nicht verpflichtet ist, nämlich
2. ☐ Ansprüche Nr.
weil sie sich auf Teile der internationalen Anmeldung beziehen, die den vorgeschriebenen Anforderungen so wenig entsprechen, daß eine sinnvolle internationale Recherche nicht durchgeführt werden kann, nämlich
3. ☐ Ansprüche Nr.
weil es sich dabei um abhängige Ansprüche handelt, die nicht entsprechend Satz 2 und 3 der Regel 6.4 a) abgefaßt sind.

Feld II Bemerkungen bei mangelnder Einheitlichkeit der Erfindung (Fortsetzung von Punkt 3 auf Blatt 1)

Die internationale Recherchenbehörde hat festgestellt, daß diese internationale Anmeldung mehrere Erfindungen enthält:

siehe Zusatzblatt

1. ☐ Da der Anmelder alle erforderlichen zusätzlichen Recherchegebühren rechtzeitig entrichtet hat, erstreckt sich dieser internationale Recherchenbericht auf alle recherchierbaren Ansprüche.
2. ☐ Da für alle recherchierbaren Ansprüche die Recherche ohne einen Arbeitsaufwand durchgeführt werden konnte, der eine zusätzliche Recherchegebühr gerechtfertigt hätte, hat die Behörde nicht zur Zahlung einer solchen Gebühr aufgefordert.
3. ☐ Da der Anmelder nur einige der erforderlichen zusätzlichen Recherchegebühren rechtzeitig entrichtet hat, erstreckt sich dieser internationale Recherchenbericht nur auf die Ansprüche, für die Gebühren entrichtet worden sind, nämlich auf die Ansprüche Nr.
4. ☒ Der Anmelder hat die erforderlichen zusätzlichen Recherchegebühren nicht rechtzeitig entrichtet. Der internationale Recherchenbericht beschränkt sich daher auf die in den Ansprüchen zuerst erwähnte Erfindung; diese ist in folgenden Ansprüchen erfaßt:
1-21 (alle teilweise)

Bemerkungen hinsichtlich eines Widerspruchs

- ☐ Die zusätzlichen Gebühren wurden vom Anmelder unter Widerspruch gezahlt.
- ☐ Die Zahlung zusätzlicher Recherchegebühren erfolgte ohne Widerspruch.

WEITERE ANGABEN

PCT/ISA/ 210

Die internationale Recherchenbehörde hat festgestellt, dass diese internationale Anmeldung mehrere (Gruppen von) Erfindungen enthält, nämlich:

1. Ansprüche: 1-21 (alle teilweise)

Erfindungen 1-1500

Array bestehend aus mindestens eines der in Tabellen 1-6 aufgeführten Gene; und verwendung des Arrays,

wo die Sequenz des Gens entsprechendes Genbank accession no. ist:

-für Erfindung 1: M17565.1

-für Erfindung 2: X00452.1

-für Erfindungen 3-1500: BF338947-NM_015957.1
